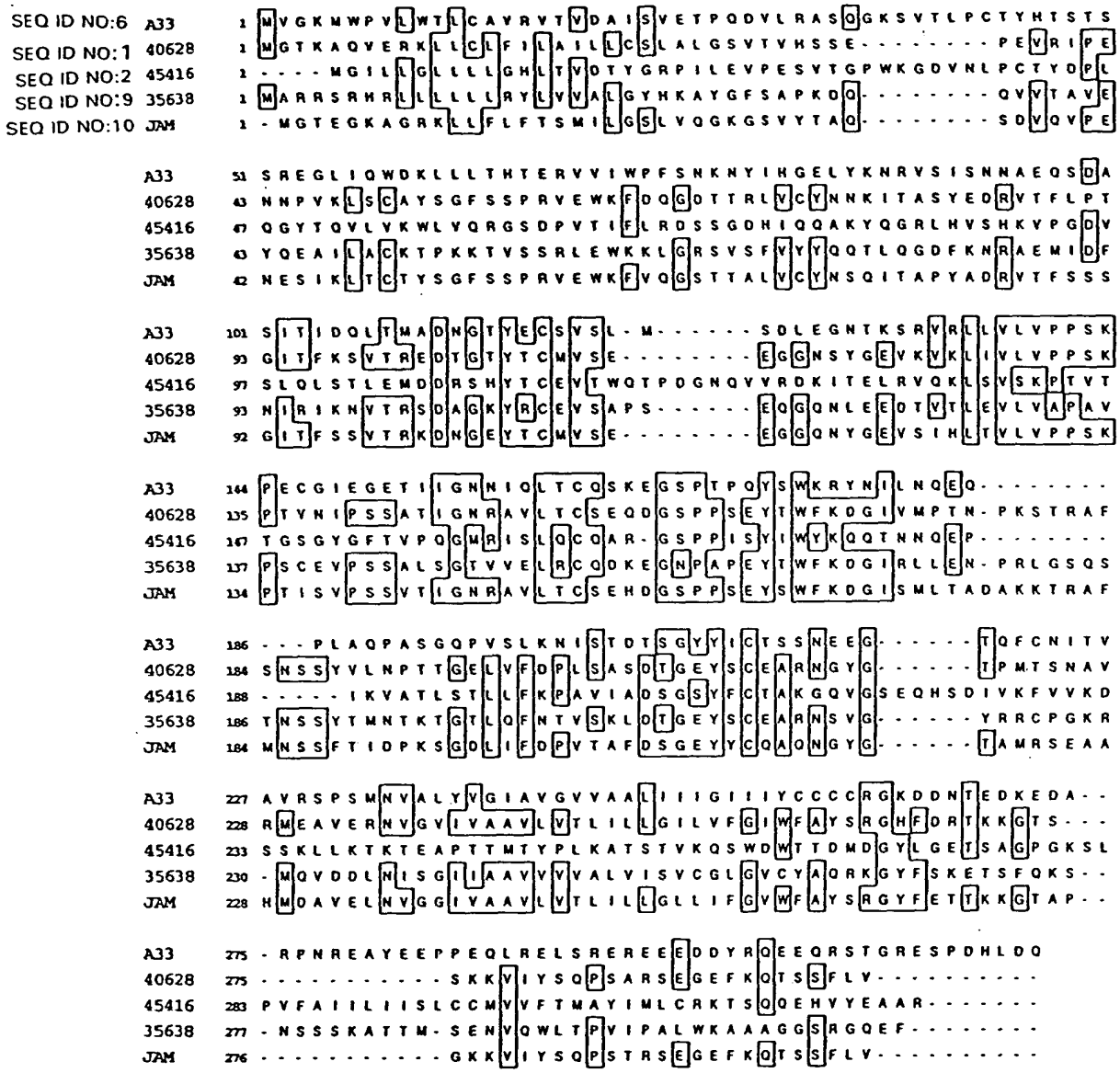

SEQ ID NO:6 A33
SEQ ID NO:1 40628
SEQ ID NO:2 45416
SEQ ID NO:9 35638
SEQ ID NO:10 JAM

Figure 1

SEQ ID NO:1

```
Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr
  1               5                  10                  15                  20                  25                  30

Val His Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val
                 35                  40                  45                  50                  55                  60

Glu Trp Lys Phe Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu
                 65                  70                  75                  80                  85                  90

Pro Thr Gly Ile Thr Phe Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser Glu Glu Gly Gly Asn Ser Tyr Gly
                 95                 100                 105                 110                 115                 120

Glu Val Lys Val Lys Leu Ile Val Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr Ile Gly Asn Arg Ala Val
                125                 130                 135                 140                 145                 150

Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn Pro Lys Ser Thr
                155                 160                 165                 170                 175                 180

Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly Glu Tyr
                185                 190                 195                 200                 205                 210

Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val
                215                 220                 225                 230                 235                 240

Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys
                245                 250                 255                 260                 265                 270

Lys Gly Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val
                275                 280                 285                 290                 295             299
```

Figure 2

SEQ ID NO:2

1 MGILLGLLLL GHLTVDTYGR PILEVPESVT GPWKGDVNLP CTYDPLQGYT QVLVKWLVQR GSDPVTIFLR DSSGDHIQQA KYQGRLHVSH KVPGDVSLQL

101 STLEMDDRSH YTCEVTWQTP DGNQVVRDKI TELRVQKLSV SKPTVTTGSG YGFTVPQGMR ISLQCQARGS PPISYIWYKQ QTNNQEPIKV ATLSTLLFKP
^Glycosaminoglycan attachment site

201 AVIADSGSYF CTAKGQVGSE QHSDIVKFVV KDSSKLLKTK TEAPTTMTYP LKATSTVKQS WDWTTDMDGY LGETSAGPGK SLPVFAIILI ISLCCMVVFT
^Transmembrane domain

301 MAYIMLCRKT SQQEHVYEAA R

Figure 3

DNA35936 (SEQ ID NO: 3)

CTTCTTGCCA ACTGGTATCA CCTTCAAGTC CGTGACACGG GAAGACACTG 50
GGACATACAC TTGTATGGTC TCTGAGGAAG GCGGCAACAG CTATGGGGAG 100
GTCAAGGTCA AGCTCATCGT GCTTGTGCCT CCATCCAAGC CTACAGTTAA 150
CATCCCCTCC TCTGCCACCA TTGGGAACCG GGCAGTGCTG ACATGCTCAG 200
AACAAGATGG TTCCCCACCT TCTGAATACA CCTGGTTCAA AGATGGGATA 250
GTGATGCCTA CGAATCCCAA AAGCACCCGT GCCTTCAGCA ACTCTTCCTA 300
TGTCCTGAAT CCCACAACAG GAGAGCTGGT CTTTGATCCC CTGTCAGCCT 350
CTGATACTGG AGAATACAGC TGTGAGGCAC GGAATGGGTA 390

Figure 4A

consen01 (SEQ ID NO: 4)

TCTCAGTCCC CTCGCTGTAG TCGCGGAGCT GTGTTCTGTT TCCCAGGAGT 50
CCTTCGGCGG CTGTTGTGCT CAGGTGCGCC TGATCGCGAT GGGGACAAAG 100
GCGCAAGCTC GAGAGGAAAC TGTTGTGCCT CTTCATATTG GCGATCCTGT 150
TGTGCTCCCT GGCATTGGGC AGTGTTACAG TTGCACTCTT CTGAACCTGA 200
AGTCAGAATT CCTGAGAATA ATCCTGTGAA GTTGTCCTGT GCCTACTCGG 250
GCTTTTCTTC TCCCCGTGTG GAGTGGAAGT TTGACCAAGG AGACACCACC 300
AGACTCGTTT GCTATAATAA CAAGATCACA GCTTCCTATG AGGACCGGGT 350
GACCTTCTTG CCAACTGGTA TCACCTTCAA GTCCGTGACA CGGGAAGACA 400
CTGGGACATA CACTTGTATG GTCTCTGAGG AAGGCGGCAA CAGCTATGGG 450
GAGGTCAAGG TCAAGCTCAT CGTGCTTGTG CCTCCATCCA AGCCTACAGT 500
TAACATCCCC TCCTCTGCCA CCATTGGGAA CCGGGCAGTG CTGACATGCT 550
CAGAACAAGA TGGTTCCCCA CCTTCTGAAT ACACCTGGTT CAAAGATGGG 600
ATAGTGATGC CTACGAATCC CAAAAGCACC CGTGCCTTCA GCAACTCTTC 650
CTATGTCCTG AATCCCACAA CAGGAGAGCT GGTCTTTGAT CCCCTGTCAG 700
CCTCTGATAC TGGAGAATAC AGCTGT 726

Figure 4B

consen02 (SEQ ID NO:5)

GCAGGCAAAG TACCAGGGCC GCCTGCATGT GAGCCACAAG GTTCCAGGAG 50
ATGTATCCCT CCAATTGAGC ACCCTGGAGA TGGATGACCG GAGCCACTAC 100
ACGTGTGAAG TCACCTGGCA GACTCCTGAT GGCAACCAAG TCGTGAGAGA 150
TAAGATTACT GAGCTCCGTG TCCAGAAACT CTCTGTCTCC AAGCCCACAG 200
TGACAACTGG CAGCGGTTAT GGCTTCACGG TGCCCCAGGG AATGAGGATT 250
AGCCTTCAAT GCCAGGGTTC GGGGTTCTCC TCCCATCAGT TATATTTGGT 300
ATAAGCAACA GACTAATAAC CAGGGAACCC ATCAAAGTAG CAACCCTAAG 350
TACCTTACTC TTCAAGCCTG CGGTGATAGC CGACTCAGGC TCCTATTTCT 400
GCACTGCCAA GGGCCAGGTT GGCTCTGAGC AGCACAGCGA CATTGTGAAG 450
TTTGTGGTCA AAGACTCCTC AAAGCTACTC AAGACCAAGA CTGAGGCACC 500
TACAACCATG ACATACCCCT TGAAAGCAAC ATCTACAGTG AAGCAGTCCT 550
GGGACTGGAC CACTGACATG GATGGCTACC TTGGAGAGAC CAGTGCTGGG 600
CCAGGAAAGA GCCTGCCTGT CTTTGCCATC ATCCTCATCA TCTCCTTGTG 650
CTGTATGGTG GTTTTTACCA TGGCCTATAT CATGCTCTGT CGGAAGACAT 700
CCCAACAAGA GCATGTCTAC GAAGCAGCCA GGGCACATGC CAGAGAGGCC 750
AACGACTCTG GAGAAACCAT GAGGGTGGCC ATCTTCGCAA GTGGCTGCTC 800
CAGTGATGAG CCAACTTCCC AGAATCTGGG GCAACAACTA CTCTGATGAG 850
CCCTGCATAG GACAGGAGTA CCAGATCATC GCCCAGATCA ATGGCAACTA 900
CGCCCGCCTG CTGGACACAG TTCCTCTGGA TTATGAGTTT CTGGCCACTG 950
AGGGCAAAAG TGTCTGTTAA AAATGCCCCA TTAGGCCAGG ATCTGCTGAC 1000
ATAATTGCCT AGTCAGTCCT TGCCTTCTGC ATGGCCTTCT TCCCTGCTAC 1050
CTCTCTTCCT GGATAGCCCA AAGTGTCCGC CTACCAACAC TGGAGCCGCT 1100
GGGAGTCACT GGCTTTGCCC TGGAATTTGC CAGATGCATC TCAAGTAAGC 1150
CAGCTGCTGG ATTTGGCTCT GGGCCCTTCT AGTATCTCTG CCGGGGGCTT 1200
CTGGTACTCC TCTCTAAATA CCAGAGGGAA GATGCCCATA GCACTAGGAC 1250
TTGGTCATCA TGCCTACAGA CACTATTCAA CTTTGGCATC TTGCCACCAG 1300
AAGACCCGAG GGGAGGCTCA GCTCTGCCAG CTCAGAGGAC CAGCTATATC 1350
CAGGATCATT TCTCTTTCTT CAGGGCCAGA CAGCTTTTAA TTGAAATTGT 1400
TATTTCACAG GCCAGGGTTC AGTTCTGCTC CTCCACTATA AGTCTAATGT 1450
TCTGACTCTC TCCTGGTGCT CAATAAATAT CTAATCATAA CAGCAAAAAA 1500
AAA 1503

Figure 4C

SEQ ID NO:11

GTCTGTTCCC AGGAGTCCTT CGGCGGCTGT TGTGTCAGTG GCCTGATCGC GATGGGGACA AAGGCGCAAG TCGAGAGGAA ACTGTTGTGC CTCTTCATAT 100

TGGCGATCCT GTTGTGCTCC CTGGCATTGG GCAGTGTTAC AGTGCACTCT TCTGAACCTG AAGTCAGAAT TCCTGAGAAT AATCCTGTGA AGTTGTCCTG 200

TGCCTACTCG GGCTTTTCTT CTCCCCGTGT GGAGTGGAAG TTTGACCAAG GAGACACCAC CAGACTCGTT TGCTATAATA ACAAGATCAC AGCTTCCTAT 300

GAGGACCGGG TGACCTTCTT GCCAACTGGT ATCACCTTCA AGTCCGTGAC ACGGGAAGAC ACTGGGACAT ACACTTGTAT GGTCTCTGAG GAAGGCGGCA 400

ACAGCTATGG GGAGGTCAAG GTCAAGCTCA TCGTGCTTGT GCCTCCATCC AAGCCTACAG TTAACATCCC CTCCTCTGCC ACCATTGGGA ACCGGGCAGT 500

GCTGACATGC TCAGAACAAG ATGGTTCCCC ACCTTCTGAA TACACCTGGT TCAAAGATGG GATAGTGATG CCTACGAATC CCAAAAGCAC CCGTGCCTTC 600

AGCAACTCTT CCTATGTCCT GAATCCCACA ACAGGAGAGC TGGTCTTTGA TCCCCTGTCA GCCTCTGATA CTGGAGAATA CAGCTGTGAG GCACGGAATG 700

GGTATGGGAC ACCCATGACT TCAAATGCTG TGCGCATGGA AGCTGTGGAG CGGAATGTGG GGGTCATCGT GGCAGCCGTC CTTGTAACCC TGATTCTCCT 800

GGGAATCTTG GTTTTTGGCA TCTGGTTTGC CTATAGCCGA GGCCACTTTG ACAGAACAAA GAAAGGGACT TCGAGTAAGA AGGTGATTTA CAGCCAGCCT 900

AGTGCCCGAA GTGAAGGAGA ATTCAAACAG ACCTCGTCAT TCCTGGTGTG AGCCTGGTCG GCTCACCGCC TATCATCTGC ATTTGCCTTA CTCAGGTGCT 1000

ACCGGACTCT GGCCCCTGAT GTCTGTAGTT TCACAGGATG CCTTATTTGT CTTCTACACC CCACAGGGCC CCCTACTTCT TCGGATGTGT TTTTAATAAT 1100

GTCAGCTATG TGCCCCATCC TCCTTCATGC CCTCCCTCCC TTTCCTACCA CTGCTGAGTG GCCTGGAACT TGTTTAAAGT GTTTATTCCC CATTTCTTTG 1200

AGGGATCAGG AAGGAATCCT GGGTATGCCA TTGACTTCCC TTCTAAGTAG ACAGCAAAAA TGGCGGGGGT CGCAGGAATC TGCACTCAAC TGCCCACCTG 1300

GCTGGCAGGG ATCTTTGAAT AGGTATCTTG AGCTTGGTTC TGGGCTCTTT CCTTGTGTAC TGACGACCAG GGCCAGCTGT TCTAGAGCGG GAATTAGAGG 1400

CTAGAGCGGC TGAAATGGTT GTTTGGTGAT GACACTGGGG TCCTTCCATC TCTGGGGCCC ACTCTCTTCT GTCTTCCCAT GGGAAGTGCC ACTGGGATCC 1500

CTCTGCCCTG TCCTCCTGAA TACAAGCTGA CTGACATTGA CTGTGTCTGT GGAAAATGGG AGCTCTTGTT GTGGAGAGCA TAGTAAATTT TCAGAGAACT 1600

TGAAGCCAAA AGGATTTAAA ACCGCTGCTC TAAAGAAAAG AAAACTGGAG GCTGGGCGCA GTGGCTCACG CCTGTAATCC CAGAGGCTGA GGCAGGCGGA 1700

TCACCTGAGG TCGGGAGTTC GGGATCAGCC TGACCAACAT GGAGAAACCC TACTGGAAAT ACAAAGTTAG CCAGGCATGG TGGTGCATGC CTGTAGTCCC 1800

AGCTGCTCAG GAGCCTGGCA ACAAGAGCAA AACTCCAGCT CA 1842

Figure 5

SEQ ID NO:7

```
  1 CCCACGCGTC CGCCCACGCG TCCGCCCACG GGTCCGCCCA CGCGTCCGGG CCACCAGAAG TTTGAGCCTC TTTGGTAGCA GGAGGCTGGA AGAAAGGACA
    GGGTGCGCAG GCGGGTGCGC AGGCGGGTGC CCAGGCGGGT GCGCAGGCCC GGTGGTCTTC AAACTCGGAG AAACCATCGT CCTCCGACCT TCTTTCCTGT

101 GAAGTAGCTC TGGCTGTGAT GGGGATCTTA CTGGGCCTGC TACTCCTGGG GCACCTAACA GTGGACACTT ATGGCCGTCC CATCCTGGAA GTGCCAGAGA
    CTTCATCGAG ACCGACACTA CCCCTAGAAT GACCCGGACG ATGAGGACCC CGTGGATTGT CACCTGTGAA TACCGGCAGG GTAGGACCTT CACGGTCTCT
  1         SEQ ID NO:2 M   G I L   L G L L   L L G   H L T   V D T Y   G R P   I L E   V P E S
                        ^MET

201 GTGTAACAGG ACCTTGGAAA GGGGATGTGA ATCTTCCCTG CACCTATGAC CCCCTGCAAG GCTACACCCA AGTCTTGGTG AAGTGGCTGG TACAACGTGG
    CACATTGTCC TGGAACCTTT CCCCTACACT TAGAAGGGAC GTGGATACTG GGGGACGTTC CGATGTGGGT TCAGAACCAC TTCACCGACC ATGTTGCACC
 29   V T G   P W K   G D V N   L P C   T Y D   P L Q G   Y T Q   V L V   K W L V   Q R G

301 CTCAGACCCT GTCACCATCT TTCTACGTGA CTCTTCTGGA GACCATATCC AGCAGGCAAA GTACCAGGGC CGCCTGCATG TGAGCCACAA GGTTCCAGGA
    GAGTCTGGGA CAGTGGTAGA AAGATGCACT GAGAAGACCT CTGGTATAGG TCGTCCGTTT CATGGTCCCG GCGGACGTAC ACTCGGTGTT CCAAGGTCCT
 62  S D P   V T I F   L R D   S S G   D H I Q   Q A K   Y Q G   R L H V   S H K   V P G

401 GATGTATCCC TCCAATTGAG CACCCTGGAG ATGGATGACC GGAGCCACTA CACGTGTGAA GTCACCTGGC AGACTCCTGA TGGCAACCAA GTCGTGAGAG
    CTACATAGGG AGGTTAACTC GTGGGACCTC TACCTACTGG CCTCGGTGAT GTGCACACTT CAGTGGACCG TCTGAGGACT ACCGTTGGTT CAGCACTCTC
 95 D V S L   Q L S   T L E   M D D R   S H Y   T C E   V T W Q   T P D   G N Q   V V R D

501 ATAAGATTAC TGAGCTCCGT GTCCAGAAAC TCTCTGTCTC CAAGCCCACA GTGACAACTG GCAGCGGTTA TGGCTTCACG GTGCCCCAGG GAATGAGGAT
    TATTCTAATG ACTCGAGGCA CAGGTCTTTG AGAGACAGAG GTTCGGGTGT CACTGTTGAC CGTCGCCAAT ACCGAAGTGC CACGGGGTCC CTTACTCCTA
129   K I T   E L R   V Q K L   S V S   K P T   V T T G   S G Y   G F T   V P Q G   M R I

601 TAGCCTTCAA TGCCAGGCTC GGGGTTCTCC TCCCATCAGT TATATTTGGT ATAAGCAACA GACTAATAAC CAGGAACCCA TCAAAGTAGC AACCCTAAGT
    ATCGGAAGTT ACGGTCCGAG CCCCAAGAGG AGGGTAGTCA ATATAAACCA TATTCGTTGT CTGATTATTG GTCCTTGGGT AGTTTCATCG TTGGGATTCA
162  S L Q   C Q A R   G S P   P I S   Y I W Y   K Q Q   T N N   Q E P I   K V A   T L S

701 ACCTTACTCT TCAAGCCTGC GGTGATAGCC GACTCAGGCT CCTATTTCTG CACTGCCAAG GGCCAGGTTG GCTCTGAGCA GCACAGCGAC ATTGTGAAGT
    TGGAATGAGA AGTTCGGACG CCACTATCGG CTGAGTCCGA GGATAAAGAC GTGACGGTTC CCGGTCCAAC CGAGACTCGT CGTGTCGCTG TAACACTTCA
195 T L L F   K P A   V I A   D S G S   Y F C   T A K   G Q V G   S E Q   H S D   I V K F

801 TTGTGGTCAA AGACTCCTCA AAGCTACTCA AGACCAAGAC TGAGGCACCT ACAACCATGA CATACCCCTT GAAAGCAACA TCTACAGTGA AGCAGTCCTG
    AACACCAGTT TCTGAGGAGT TTCGATGAGT TCTGGTTCTG ACTCCGTGGA TGTTGGTACT GTATGGGGAA CTTTCGTTGT AGATGTCACT TCGTCAGGAC
229   V V K   D S S   K L L K   T K T   E A P   T T M T   Y P L   K A T   S T V K   Q S W
```

Figure 6A

```
SEQ ID NO:7  901 GGACTGGACC ACTGACATGG ATGGCTACCT TGGAGAGACC AGTGCTGGGC CAGGAAAGAG CCTGCCTGTC TTTGCCATCA TCCTCATCAT CTCCTTGTGC
             CCTGACCTGG TGACTGTACC TACCGATGGA ACCTCTCTGG TCACGACCCG GTCCTTTCTC GGACGGACAG AAACGGTAGT AGGAGTAGTA GAGGAACACG
SEQ ID NO:2  262  D  W  T   T  D  M  D   G  Y  L   G  E  T   S  A  G  P   G  K  S   L  P  V   F  A  I  I   L  I  I   S  L  C

            1001 TGTATGGTGG TTTTTACCAT GGCCTATATC ATGCTCTGTC GGAAGACATC CCAACAAGAG CATGTCTACG AAGCAGCCAG GTAAGAAAGT CTCTCCTCTT
                 ACATACCACC AAAAATGGTA CCGGATATAG TACGAGACAG CCTTCTGTAG GGTTGTTCTC GTACAGATGC TTCGTCGGTC CATTCTTTCA GAGAGGAGAA
             295 C  M  V  V   F  T  M   A  Y  I   M  L  C  R   K  T  S   Q  Q  E   H  V  Y  E   A  A  R   O

            1101 CCATTTTTGA CCCCGTCCCT GCCCTCAATT TTGATTACTG GCAGGAAATG TGGAGGAAGG GGGGTGTGGC ACAGACCCAA TCCTAAGGCC GGAGGCCTTC
                 GGTAAAAACT GGGGCAGGGA CGGGAGTTAA AACTAATGAC CGTCCTTTAC ACCTCCTTCC CCCCACACCG TGTCTGGGTT AGGATTCCGG CCTCCGGAAG

            1201 AGGGTCAGGA CATAGCTGCC TTCCCTCTCT CAGGCACCTT CTGAGGTTGT TTTGGCCCTC TGAACACAAA GGATAATTTA GATCCATCTG CCTTCTGCTT
                 TCCCAGTCCT GTATCGACGG AAGGGAGAGA GTCCGTGGAA GACTCCAACA AAACCGGGAG ACTTGTGTTT CCTATTAAAT CTAGGTAGAC GGAAGACGAA

            1301 CCAGAATCCC TGGGTGGTAG GATCCTGATA ATTAATTGGC AAGAATTGAG GCAGAAGGGT GGGAAACCAG GACCACAGCC CCAAGTCCCT TCTTATGGGT
                 GGTCTTAGGG ACCCACCATC CTAGGACTAT TAATTAACCG TTCTTAACTC CGTCTTCCCA CCCTTTGGTC CTGGTGTCGG GGTTCAGGGA AGAATACCCA

            1401 GGTGGGCTCT TGGGCCATAG GGCACATGCC AGAGAGGCCA ACGACTCTGG AGAAACCATG AGGGTGGCCA TCTTCGCAAG TGGCTGCTCC AGTGATGAGC
                 CCACCCGAGA ACCCGGTATC CCGTGTACGG TCTCTCCGGT TGCTGAGACC TCTTTGGTAC TCCCACCGGT AGAAGCGTTC ACCGACGAGG TCACTACTCG

            1501 CAACTTCCCA GAATCTGGGC AACAACTACT CTGATGAGCC CTGCATAGGA CAGGAGTACC AGATCATCGC CCAGATCAAT GGCAACTACG CCCGCCTGCT
                 GTTGAAGGGT CTTAGACCCG TTGTTGATGA GACTACTCGG GACGTATCCT GTCCTCATGG TCTAGTAGCG GGTCTAGTTA CCGTTGATGC GGGCGGACGA

            1601 GGACACAGTT CCTCTGGATT ATGAGTTTCT GGCCACTGAG GGCAAAAGTG TCTGTTAAAA ATGCCCCATT AGGCCAGGAT CTGCTGACAT AATTGCCTAG
                 CCTGTGTCAA GGAGACCTAA TACTCAAAGA CCGGTGACTC CCGTTTTCAC AGACAATTTT TACGGGGTAA TCCGGTCCTA GACGACTGTA TTAACGGATC

            1701 TCAGTCCTTG CCTTCTGCAT GGCCTTCTTC CCTGCTACCT CTCTTCCTGG ATAGCCCAAA GTGTCCGCCT ACCAACACTG GAGCCGCTGG GAGTCACTGG
                 AGTCAGGAAC GGAAGACGTA CCGGAAGAAG GGACGATGGA GAGAAGGACC TATCGGGTTT CACAGGCGGA TGGTTGTGAC CTCGGCGACC CTCAGTGACC

            1801 CTTTGCCCTG GAATTTGCCA GATGCATCTC AAGTAAGCCA GCTGCTGGAT TTGGCTCTGG GCCCTTCTAG TATCTCTGCC GGGGGCTTCT GGTACTCCTC
                 GAAACGGGAC CTTAAACGGT CTACGTAGAG TTCATTCGGT CGACGACCTA AACCGAGACC CGGGAAGATC ATAGAGACGG CCCCCGAAGA CCATGAGGAG

            1901 TCTAAATACC AGAGGGAAGA TGCCCATAGC ACTAGGACTT GGTCATCATG CCTACAGACA CTATTCAACT TTGGCATCTT GCCACCAGAA GACCCGAGGG
                 AGATTTATGG TCTCCCTTCT ACGGGTATCG TGATCCTGAA CCAGTAGTAC GGATGTCTGT GATAAGTTGA AACCGTAGAA CGGTGGTCTT CTGGGCTCCC

            2001 AGGCTCAGCT CTGCCAGCTC AGAGGACCAG CTATATCCAG GATCATTTCT CTTTCTTCAG GGCCAGACAG CTTTTAATTG AAATTGTTAT TTCACAGGCC
                 TCCGAGTCGA GACGGTCGAG TCTCCTGGTC GATATAGGTC CTAGTAAAGA GAAAGAAGTC CCGGTCTGTC GAAAATTAAC TTTAACAATA AAGTGTCCGG

            2101 AGGGTTCAGT TCTGCTCCTC CACTATAAGT CTAATGTTCT GACTCTCTCC TGGTGCTCAA TAAATATCTA ATCATAACAG C
                 TCCCAAGTCA AGACGAGGAG GTGATATTCA GATTACAAGA CTGAGAGAGG ACCACGAGTT ATTTATAGAT TAGTATTGTC G
```

Figure 6B

SEQ ID NO:8

CCCAGAAGTTCAAGGGCCCCCGGCCTCCTGCGCTCCTGCCGCCGGGACCCTCGACCTCCT
CAGAGCAGCCGGCTGCCGCCCCGGGAAGATGGCGAGCAGGAGCCGCCACCGCCTCCTCCT
GCTGCTGCTGCGCTACCTGGTGGTCGCCCTGGGCTATCATAAGGCCTATGGGTTTTCTGC
CCCAAAAGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTTAGCCTGCAA
AACCCCAAAGAAGACTGTTTCCTCCAGATTAGAGTGGAAGAAACTGGGTCGGAGTGTCTC
CTTTGTCTACTATCAACAGACTCTTCAAGGTGATTTTAAAAATCGAGCTGAGATGATAGA
TTTCAATATCCGGATCAAAAATGTGACAAGAAGTGATGCGGGGAAATATCGTTGTGAAGT
TAGTGCCCCATCTGAGCAAGGCCAAAACCTGGAAGAGGATACAGTCACTCTGGAAGTATT
AGTGGCTCCAGCAGTTCCATCATGTGAAGTACCCTCTTCTGCTCTGAGTGGAACTGTGGT
AGAGCTACGATGTCAAGACAAAGAAGGGAATCCAGCTCCTGAATACACATGGTTTAAGGA
TGGCATCCGTTTGCTAGAAAATCCCAGACTTGGCTCCCAAAGCACCAACAGCTCATACAC
AATGAATACAAAAACTGGAACTCTGCAATTTAATACTGTTTCCAAACTGGACACTGGAGA
ATATTCCTGTGAAGCCCGCAATTCTGTTGGATATCGCAGGTGTCCTGGGAAACGAATGCA
AGTAGATGATCTCAACATAAGTGGCATCATAGCAGCCGTAGTAGTTGTGGCCTTAGTGAT
TTCCGTTTGTGGCCTTGGTGTATGCTATGCTCAGAGGAAAGGCTACTTTTCAAAAGAAAC
CTCCTTCCAGAAGAGTAATTCTTCATCTAAAGCCACGACAATGAGTGAAAATGTGCAGTG
GCTCACGCCTGTAATCCCAGCACTTTGGAAGGCCGCGGCGGGCGGATCACGAGGTCAGGA
GTTCTAGACCAGTCTGGCCAATATGGTGAAACCCCATCTCTACTAAAATACAAAAATTAG
CTGGGCATGGTGGCATGTGCCTGCAGTTCCAGCTGCTTGGGAGACAGGAGAATCACTTGA
ACCCGGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGCCACTGCAGTCCAGCCTGGGTAA
CAGAGCAAGATTCCATCTCAAAAAATAAAATAAATAAATAAATAAATACTGGTTTTTACC
TGTAGAATTCTTACAATAAATATAGCTTGATATTC

Figure 7

OLI2162 (35936.f1)
SEQ ID NO:12

TCGCGGAGCTGTGTTCTGTTTCCC

OLI2163 (35936.p1)
SEQ ID NO:13

TGATCGCGATGGGGACAAAGGCGCAAGCTCGAGAGGAAACTGTTGTGCCT

OLI2164 (35936.f2)
SEQ ID NO:14

ACACCTGGTTCAAAGATGGG

OLI2165 (35936.r1)
SEQ ID NO:15

TAGGAAGAGTTGCTGAAGGCACGG

OLI2166 (35936.f3)
SEQ ID NO:16

TTGCCTTACTCAGGTGCTAC

OLI2167 (35936.r2)
SEQ ID NO:17

ACTCAGCAGTGGTAGGAAAG

Figure 8

SEQ ID NO:5

```
   1 GCAGGCAAAG TACCAGGGCC GCCTGCATGT GAGCCACAAG GTTCCAGGAG ATGTATCCCT CCAATTGAGC ACCCTGGAGA TGGATGACCG GAGCCACTAC
     CGTCCGTTTC ATGGTCCCGG CGGACGTACA CTCGGTGTTC CAAGGTCCTC TACATAGGGA GGTTAACTCG TGGGACCTCT ACCTACTGGC CTCGGTGATG
                                                          ^42257.f1 SEQ ID NO:18          ^42257.p1 SEQ ID NO:22

 101 ACGTGTGAAG TCACCTGGCA GACTCCTGAT GGCAACCAAG TCGTGAGAGA TAAGATTACT GAGCTCCGTG TCCAGAAACT CTCTGTCTCC AAGCCCACAG
     TGCACACTTC AGTGGACCGT CTGAGGACTA CCGTTGGTTC AGCACTCTCT ATTCTAATGA CTCGAGGCAC AGGTCTTTGA GAGACAGAGG TTCGGGTGTC

 201 TGACAACTGG CAGCGGTTAT GGCTTCACGG TGCCCCAGGG AATGAGGATT AGCCTTCAAT GCCAGGGTTC GGGGTTCTCC TCCCATCAGT TATATTTGGT
     ACTGTTGACC GTCGCCAATA CCGAAGTGCC ACGGGGTCCC TTACTCCTAA TCGGAAGTTA CGGTCCCAAG CCCCAAGAGG AGGGTAGTCA ATATAAACCA

 301 ATAAGCAACA GACTAATAAC CAGGGAACCC ATCAAAGTAG CAACCCTAAG TACCTTACTC TTCAAGCCTG CGGTGATAGC CGACTCAGGC TCCTATTTCT
     TATTCGTTGT CTGATTATTG GTCCCTTGGG TAGTTTCATC GTTGGGATTC ATGGAATGAG AAGTTCGGAC GCCACTATCG GCTGAGTCCG AGGATAAAGA

 401 GCACTGCCAA GGGCCAGGTT GGCTCTGAGC AGCACAGCGA CATTGTGAAG TTTGTGGTCA AAGACTCCTC AAAGCTACTC AAGACCAAGA CTGAGGCACC
     CGTGACGGTT CCCGGTCCAA CCGAGACTCG TCGTGTCGCT GTAACACTTC AAACACCAGT TTCTGAGGAG TTTCGATGAG TTCTGGTTCT GACTCCGTGG
                                                ^42257.r1 SEQ ID NO:20

 501 TACAACCATG ACATACCCCT TGAAAGCAAC ATCTACAGTG AAGCAGTCCT GGGACTGGAC CACTGACATG GATGGCTACC TTGGAGAGAC CAGTGCTGGG
     ATGTTGGTAC TGTATGGGGA ACTTTCGTTG TAGATGTCAC TTCGTCAGGA CCCTGACCTG GTGACTGTAC CTACCGATGG AACCTCTCTG GTCACGACCC

 601 CCAGGAAAGA GCCTGCCTGT CTTTGCCATC ATCCTCATCA TCTCCTTGTG CTGTATGGTG GTTTTTACCA TGGCCTATAT CATGCTCTGT CGGAAGACAT
     GGTCCTTTCT CGGACGGACA GAAACGGTAG TAGGAGTAGT AGAGGAACAC GACATACCAC CAAAAATGGT ACCGGATATA GTACGAGACA GCCTTCTGTA
                                                                                          ^42257.f2 SEQ ID NO:19

 701 CCCAACAAGA GCATGTCTAC GAAGCAGCCA GGGCACATGC CAGAGAGGCC AACGACTCTG GAGAAACCAT GAGGGTGGCC ATCTTCGCAA GTGGCTGCTC
     GGGTTGTTCT CGTACAGATG CTTCGTCGGT CCCGTGTACG GTCTCTCCGG TTGCTGAGAC CTCTTTGGTA CTCCCACCGG TAGAAGCGTT CACCGACGAG

 801 CAGTGATGAG CCAACTTCCC AGAATCTGGG GCAACAACTA CTCTGATGAG CCCTGCATAG GACAGGAGTA CCAGATCATC GCCCAGATCA ATGGCAACTA
     GTCACTACTC GGTTGAAGGG TCTTAGACCC CGTTGTTGAT GAGACTACTC GGGACGTATC CTGTCCTCAT GGTCTAGTAG CGGGTCTAGT TACCGTTGAT

 901 CGCCCGCCTG CTGGACACAG TTCCTCTGGA TTATGAGTTT CTGGCCACTG AGGGCAAAAG TGTCTGTTAA AAATGCCCCA TTAGGCCAGG ATCTGCTGAC
     GCGGGCGGAC GACCTGTGTC AAGGAGACCT AATACTCAAA GACCGGTGAC TCCCGTTTTC ACAGACAATT TTTACGGGGT AATCCGGTCC TAGACGACTG

1001 ATAATTGCCT AGTCAGTCCT TGCCTTCTGC ATGGCCTTCT TCCCTGCTAC CTCTCTTCCT GGATAGCCCA AAGTGTCCGC CTACCAACAC TGGAGCCGCT
     TATTAACGGA TCAGTCAGGA ACGGAAGACG TACCGGAAGA AGGGACGATG GAGAGAAGGA CCTATCGGGT TTCACAGGCG GATGGTTGTG ACCTCGGCGA
```

Figure 9A

SEQ ID NO:5

```
1101 GGGAGTCACT GGCTTTGCCC TGGAATTTGC CAGATGCATC TCAAGTAAGC CAGCTGCTGG ATTTGGCTCT GGGCCCTTCT AGTATCTCTG CCGGGGGCTT
     CCCTCAGTGA CCGAAACGGG ACCTTAAACG GTCTACGTAG AGTTCATTCG GTCGACGACC TAAACCGAGA CCCGGGAAGA TCATAGAGAC GGCCCCCGAA
                                                                                ^42257.r2  SEQ ID NO:21

1201 CTGGTACTCC TCTCTAAATA CCAGAGGGAA GATGCCCATA GCACTAGGAC TTGGTCATCA TGCCTACAGA CACTATTCAA CTTTGGCATC TTGCCACCAG
     GACCATGAGG AGAGATTTAT GGTCTCCCTT CTACGGGTAT CGTGATCCTG AACCAGTAGT ACGGATGTCT GTGATAAGTT GAAACCGTAG AACGGTGGTC

1301 AAGACCCGAG GGGAGGCTCA GCTCTGCCAG CTCAGAGGAC CAGCTATATC CAGGATCATT TCTCTTTCTT CAGGGCCAGA CAGCTTTTAA TTGAAATTGT
     TTCTGGGCTC CCCTCCGAGT CGAGACGGTC GAGTCTCCTG GTCGATATAG GTCCTAGTAA AGAGAAAGAA GTCCCGGTCT GTCGAAAATT AACTTTAACA

1401 TATTTCACAG GCCAGGGTTC AGTTCTGCTC CTCCACTATA AGTCTAATGT TCTGACTCTC TCCTGGTGCT CAATAAATAT CTAATCATAA CAGCAAAAAA
     ATAAAGTGTC CGGTCCCAAG TCAAGACGAG GAGGTGATAT TCAGATTACA AGACTGAGAG AGGACCACGA GTTATTTATA GATTAGTATT GTCGTTTTTT

1501 AAA
     TTT
```

Figure 9B

		Frame	Score	Match	Pct
A33_human	A33 antigen precursor - Homo sapiens	+1	246	81	30

A33_human - A33 antigen precursor - Homo sapiens (319 aa)
Score = 246 (86.6 bits), Expect = 2.8e-19, P = 2.8e-19
Identities = 81/268 (30%), Positives = 131/268 (48%), at 121,17, Frame = +1

```
DNA40628   121 LALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPR---VEW-KFDQGDTTRLVC--YNN
SEQ ID NO:23
               . . ...* . .  .*  .   * * * *   .* *   ..* *     * *.*   ..*
A33_human   17 VTVDAISVETPQDVLRASQGKSVTLPCTYHTSTSSREGLIQWDKLLLTHTERVVIWPFSN
SEQ ID NO:24

DNA40628   283 K--ITAS-YEDRVTFL------PTGITFKSVTREDTGTYTCMVS---EEGGNSYGEVKVK
               *  *    *..**.           **   .*  * *** * **   .  **.  . .*.
A33_human   77 KNYIHGELYKNRVSISNNAEQSDASITIDQLTMADNGTYECSVSLMSDLEGNT--KSRVR

DNA40628   427 LIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKSTRAFSN
               *.********   *     ***   ***  ..***  .*.* .  *.    *
A33_human  135 LLVLVPPSKPECGIEGETIIGNNIQLTCQSKEGSPTPQYSWKRYNILNQEQP--------

DNA40628   607 SSYVLNPTTGELV-FDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGV---IVA
                 . * .*. *    .*   .* * * . * **   . * . .   ** .   *
A33_human  187 ---LAQPASGQPVSLKNISTDTSGYYICTSSNEEGTQFCNITVAVRSPSMNVALYVGIAV

DNA40628   775 AVLVTLILLGILVFGIWFAYSRGHFDRT--KKGTSSKKVIYSQP
                *.  **..**...       **  * *  *.     .  * .*
A33_human  244 GVVAALIIIGIIIY---CCCCRGKDDNTEDKEDARPNREAYEEP
```

Figure 10A

Score = 245 (86.2 bits), Expect = 3.6e-19, P = 3.6e-19
Identities = 83/273 (30%), Positives = 131/273 (47%), at 112,12, Frame = +1

```
DNA40628   112 LCSL--ALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPR---VEW-KFDQGDTTRLVC
SEQ ID NO:25
               **..   . ...* . .  .*  .   * * * *   .* *   ..* *     * *.*
A33 human   12 LCAVRVTVDAISVETPQDVLRASQGKSVTLPCTYHTSTSSREGLIQWDKLLLTHTERVVI
SEQ ID NO:26

DNA40628   274 --YNNK--ITAS-YEDRVTFL------PTGITFKSVTREDTGTYTCMVSEEGGNSYGEVK
                 ..**  *    *..**.           **   .*  * *** * **    .  *  *
A33_human   72 WPFSNKNYIHGELYKNRVSISNNAEQSDASITIDQLTMADNGTYECSVSLMS-DLEGNTK

DNA40628   421 --VKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKSTR
                 *.*.********   *     ***   ***  ..***  .*.* .  *.    *
A33_human  131 SRVRLLVLVPPSKPECGIEGETIIGNNIQLTCQSKEGSPTPQYSWKRYNILNQEQP----

DNA40628   595 AFSNSSYVLNPTTGELV-FDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGV--
                     .  * .*. *    .*   .* * * . * **   .  * . .   ** .
A33_human  187 -------LAQPASGQPVSLKNISTDTSGYYICTSSNEEGTQFCNITVAVRSPSMNVALYV

DNA40628   766 -IVAAVLVTLILLGILVFGIWFAYSRGHFDRT--KKGTSSKKVIYSQP
                *   *.  **..**...       **  * *  *.     .  * .*
A33_human  240 GIAVGVVAALIIIGIIIY---CCCCRGKDDNTEDKEDARPNREAYEEP
```

Figure 10B

SEQ ID NO:9

MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTVSSR
LEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQN
LEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPR
LGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGI
IAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENVQWLTPVIPALW
KAAAGGSRGQEF

Figure 11

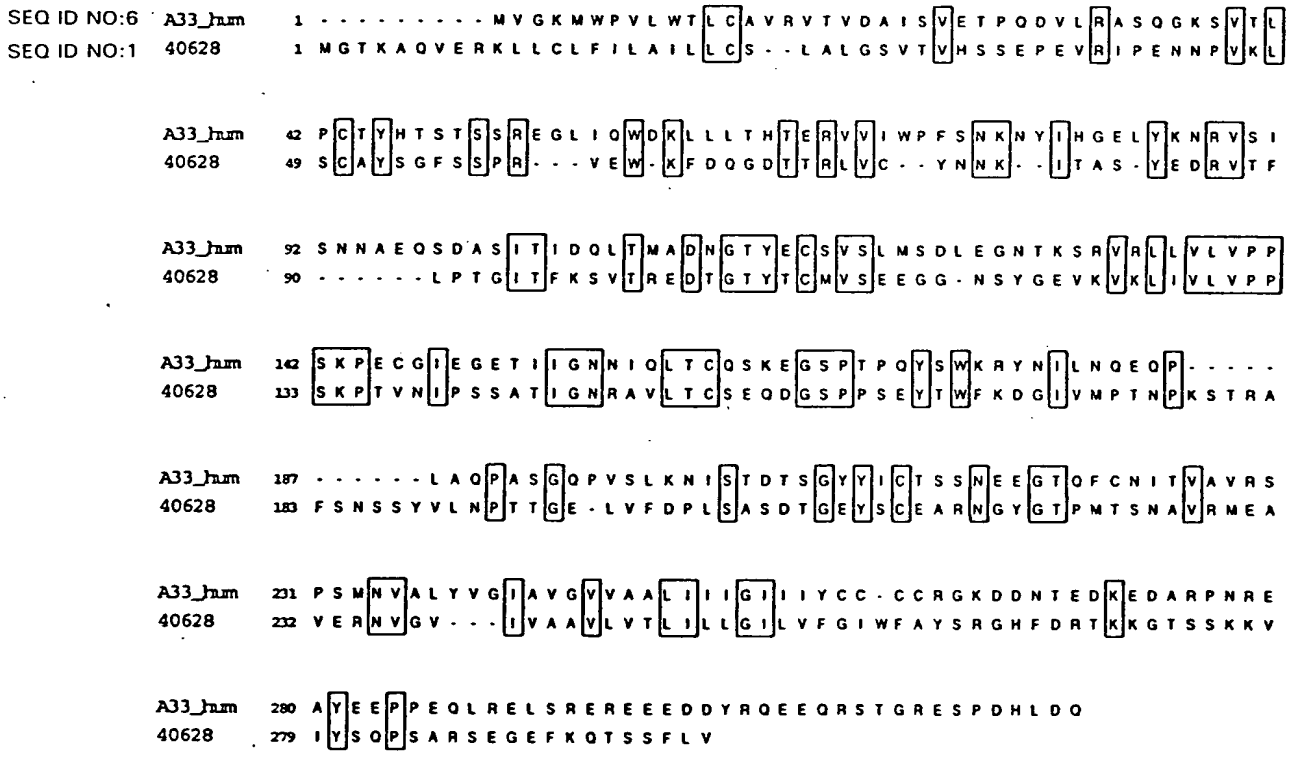


Figure 12

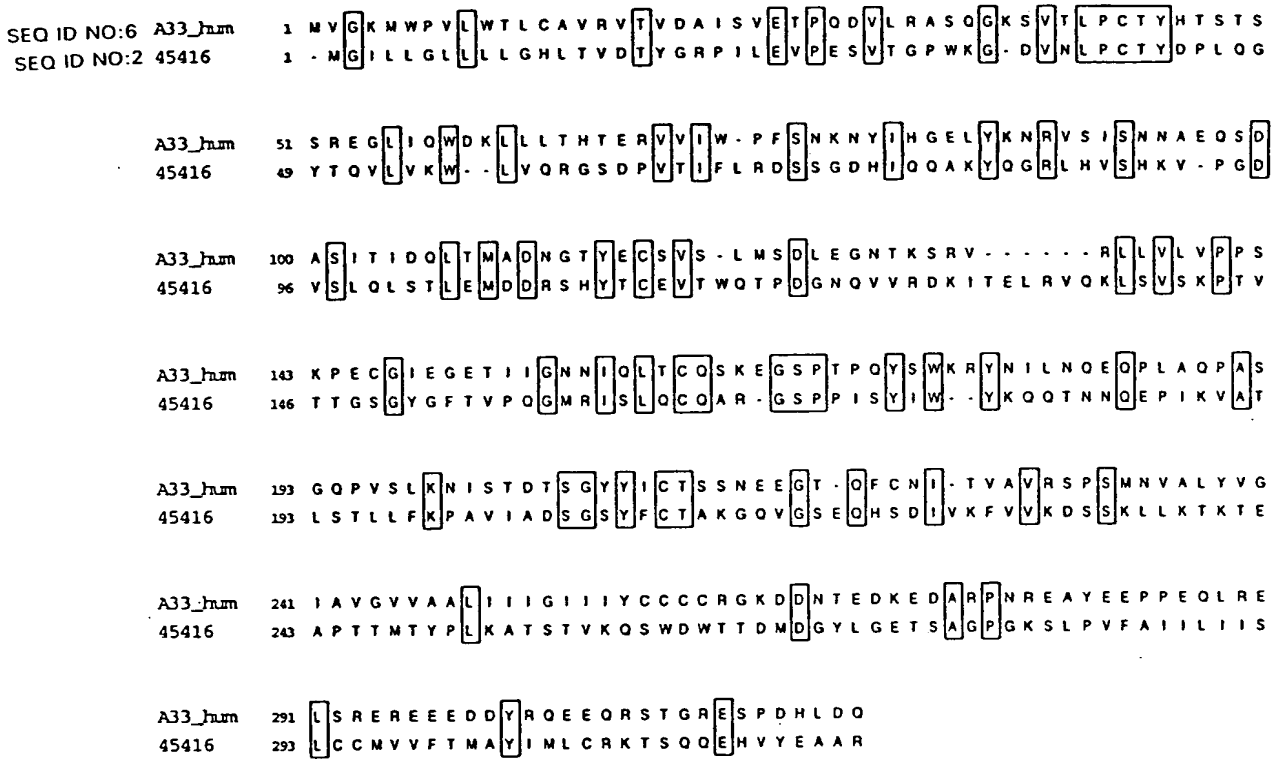

SEQ ID NO:6 A33_hum
SEQ ID NO:2 45416
A33_hum
45416
A33_hum
45416
A33_hum
45416
A33_hum
45416
A33_hum
45416
A33_hum
45416

Figure 13

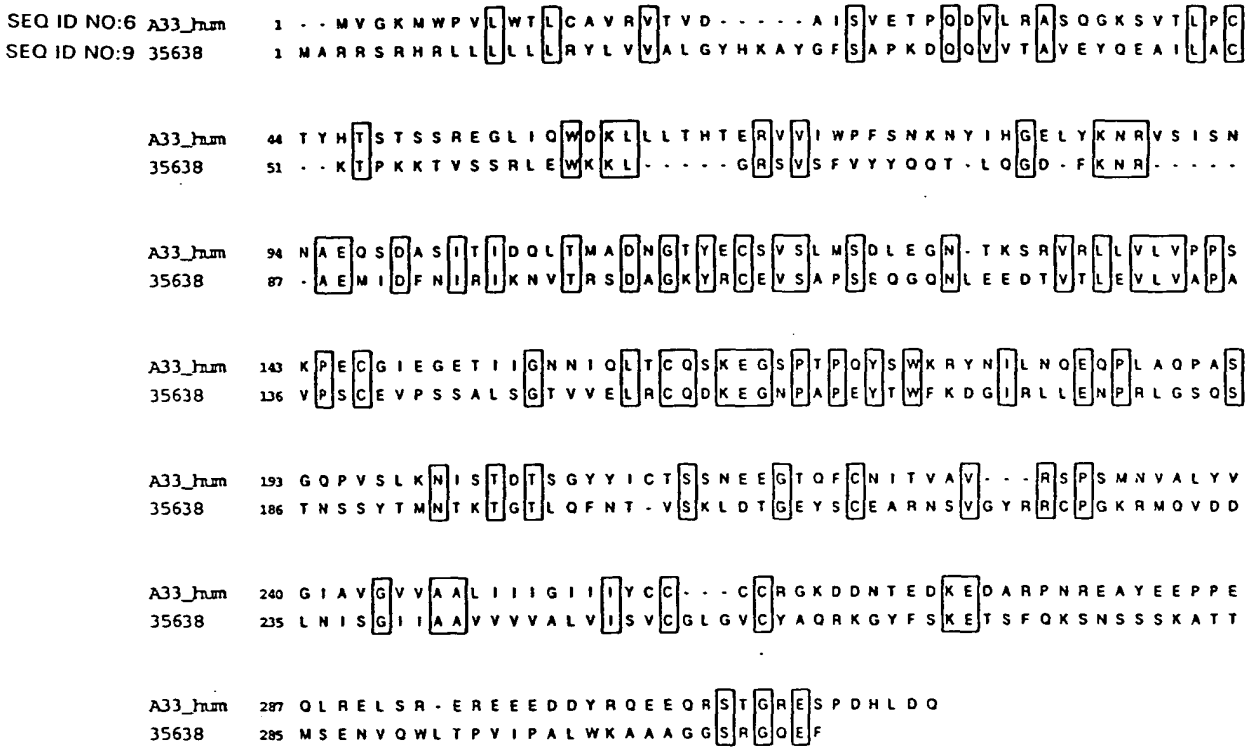
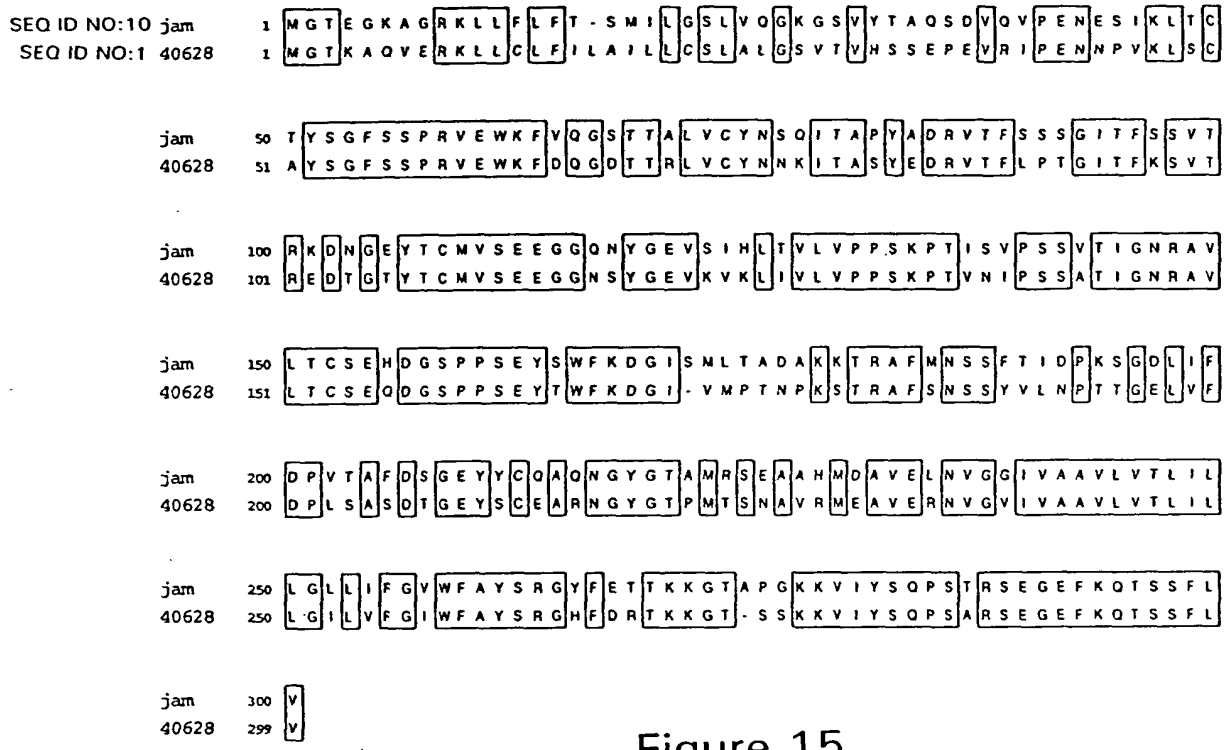

SEQ ID NO:6 A33_hum 1 - - M V G K M W P V L W T L C A V R V T V D - - - - - A I S V E T P Q D V L R A S Q G K S V T L P C
SEQ ID NO:9 35638 1 M A R R S R H R L L L L L L R Y L V V A L G Y H K A Y G F S A P K D Q Q V V T A V E Y Q E A I L A C
A33_hum 44 T Y H T S T S S R E G L I Q W D K L L L T H T E R V V I W P F S N K N Y I H G E L Y K N R V S I S N
35638 51 - - K T P K K T V S S R L E W K K L - - - - - G R S V S F V Y Y Q Q T - L Q G D - F K N R - - - - -
A33_hum 94 N A E Q S D A S I T I D Q L T M A D N G T Y E C S V S L M S D L E G N - T K S R V R L L V L V P P S
35638 87 - A E M I D F N I R I K N V T R S D A G K Y R C E V S A P S E Q G Q N L E E D T V T L E V L V A P A
A33_hum 143 K P E C G I E G E T I I G N N I Q L T C Q S K E G S P T P Q Y S W K R Y N I L N Q E Q P L A Q P A S
35638 136 V P S C E V P S S A L S G T V V E L R C Q D K E G N P A P E Y T W F K D G I R L L E N P R L G S Q S
A33_hum 193 G Q P V S L K N I S T D T S G Y Y I C T S S N E E G T Q F C N I T V A V - - - R S P S M N V A L Y V
35638 186 T N S S Y T M N T K T G T L Q F N T - V S K L D T G E Y S C E A R N S V G Y R R C P G K R M Q V D D
A33_hum 240 G I A V G V V A A L I I I G I I I Y C C - - - C C R G K D D N T E D K E D A R P N R E A Y E E P P E
35638 235 L N I S G I I A A V V V V A L V I S V C G L G V C Y A Q R K G Y F S K E T S F Q K S N S S S K A T T
A33_hum 287 Q L R E L S R - E R E E E D D Y R Q E E Q R S T G R E S P D H L D Q
35638 285 M S E N V Q W L T P V I P A L W K A A A G G S R G Q E F

Figure 14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SEQ ID NO:1 40628 1 MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSC
jam 50 TYSGFSSPRVEWKFVQGSTTALVCYNSQITAPYADRVTFSSSGITFSSVT
40628 51 AYSGFSSPRVEWKFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVT
jam 100 RKDNGEYTCMVSEEGGQNYGEVSIHLTVLVPPSKPTISVPSSVTIGNRAV
40628 101 REDTGTYTCMVSEEGGNSYGEVKVKLIVLVPPSKPTVNIPSSATIGNRAV
jam 150 LTCSEHDGSPPSEYSWFKDGISMLTADAKKTRAFMNSSFTIDPKSGDLIF
40628 151 LTCSEQDGSPPSEYTWFKDGI-VMPTNPKSTRAFSNSSYVLNPTTGELVF
jam 200 DPVTAFDSGEYYCQAQNGYGTAMRSEAAHMDAVELNVGGIVAAVLVTLIL
40628 200 DPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVAAVLVTLIL
jam 250 LGLLIFGVWFAYSRGYFETTKKGTAPGKKVIYSQPSTRSEGEFKQTSSFL
40628 250 LGILVFGIWFAYSRGHFDRTKKGT-SSKKVIYSQPSARSEGEFKQTSSFL
jam 300 V
40628 299 V

Figure 15

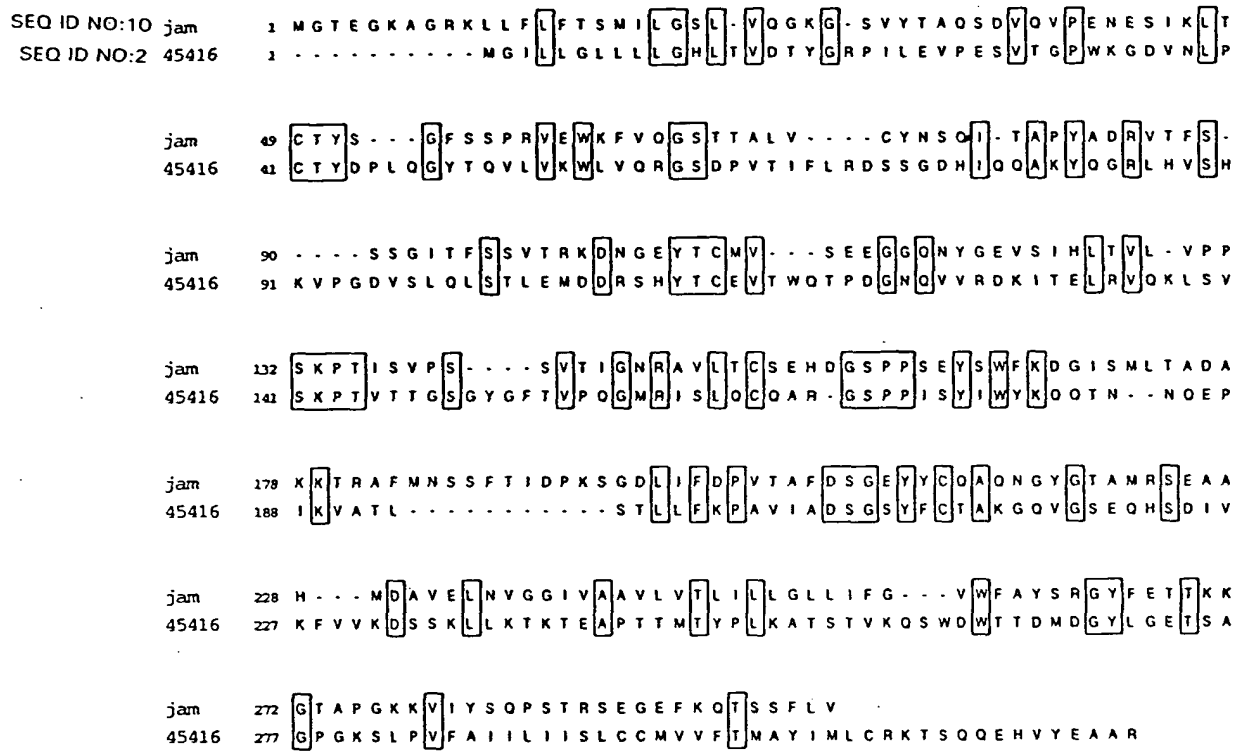

SEQ ID NO:10 jam 1 MGTEGKAGRKLLFLFTSMILGSL-VQGKG-SVYTAQSDVQVPENESIKLT
SEQ ID NO:2 45416 1 ----------MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLP
jam 49 CTYS---GFSSPRVEWKFVQGSTTALV----CYNSQI-TAPYADRVTFS-
45416 41 CTYDPLQGYTQVLVKWLVQRGSDPVTIFLRDSSGDHIQQAKYQGRLHVSH
jam 90 ----SSGITFSSVTRKDNGEYTCMV---SEEGGQNYGEVSIHLTVL-VPP
45416 91 KVPGDVSLQLSTLEMDDRSHYTCEVTWQTPDGNQVVRDKITELRVQKLSV
jam 132 SKPTISVPS----SVTIGNRAVLTCSEHDGSPPSEYSWFKDGISMLTADA
45416 141 SKPTVTTGSGYGFTVPQGMRISLQCQAR-GSPPISYIWYKQQTN--NQEP
jam 178 KKTRAFMNSSFTIDPKSGDLIFDPVTAFDSGEYYCQAQNGYGTAMRSEAA
45416 188 IKVATL----------STLLFKPAVIADSGSYFCTAKGQVGSEQHSDIV
jam 228 H---MDAVELNVGGIVAAVLVTLILLGLLIFG---VWFAYSRGYFETTKK
45416 227 KFVVKDSSKLLKTKTEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSA
jam 272 GTAPGKKVIYSQPSTRSEGEFKQTSSFLV
45416 277 GPGKSLPVFAIILIISLCCMVVFTMAYIMLCRKTSQQEHVYEAAR

Figure 16

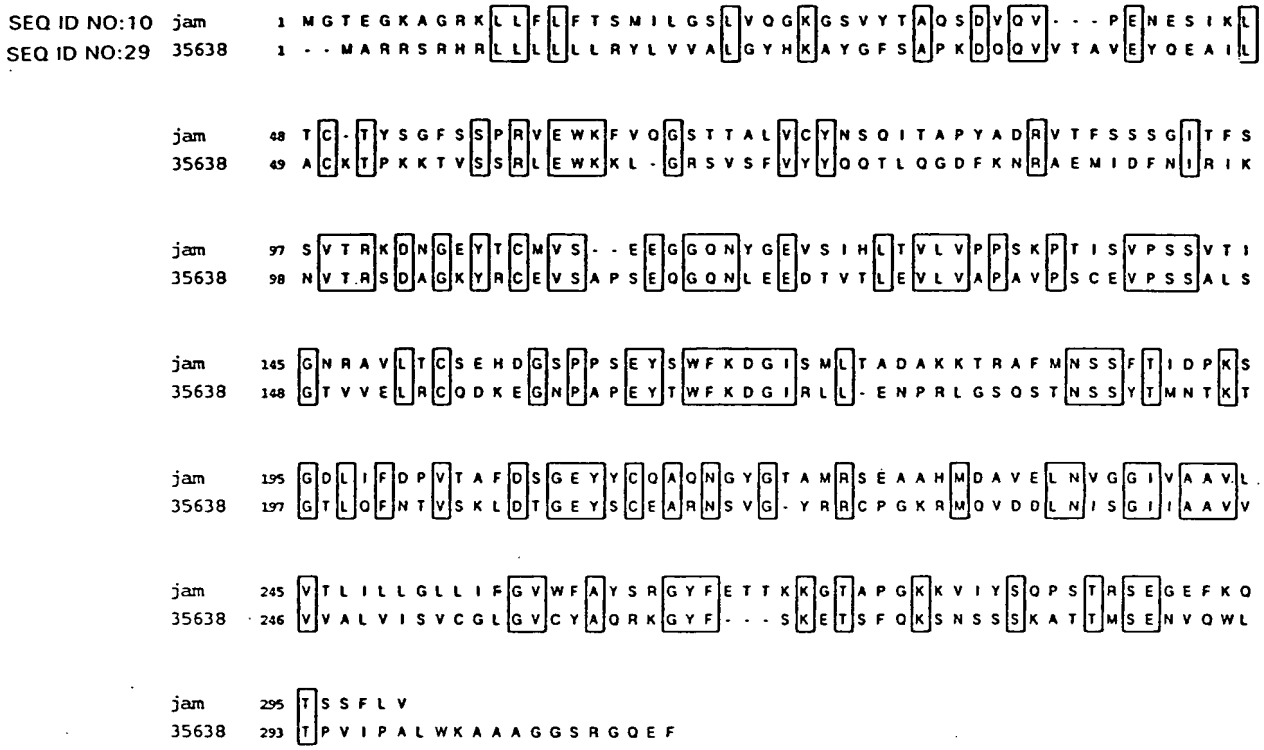

SEQ ID NO:10 jam 1 MGTEGKAGRKLLFLFTSMILGSLVQGKGSVYTAQSDVQV---PENESIKL
SEQ ID NO:29 35638 1 --MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAIL
jam 48 TC-TYSGFSSPRVEWKFVQGSTTALVCYNSQITAPYADRVTFSSSGITFS
35638 49 ACKTPKKTVSSRLEWKKL-GRSVSFVYYQQTLQGDFKNRAEMIDFNIRIK
jam 97 SVTRKDNGEYTCMVS--EEGGQNYGEVSIHLTVLVPPSKPTISVPSSVTI
35638 98 NVTRSDAGKYRCEVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVPSSALS
jam 145 GNRAVLTCSEHDGSPPSEYSWFKDGISMLTADAKKTRAFMNSSFTIDPKS
35638 148 GTVVELRCQDKEGNPAPEYTWFKDGIRLL-ENPRLGSQSTNSSYTMNTKT
jam 195 GDLIFDPVTAFDSGEYYCQAQNGYGTAMRSEAAHMDAVELNVGGIVAAVL
35638 197 GTLQFNTVSKLDTGEYSCEARNSVG-YRRCPGKRMQVDDLNISGIIAAVV
jam 245 VTLILLGLLIFGVWFAYSRGYFETTKKGTAPGKKVIYSQPSTRSEGEFKQ
35638 246 VVALVISVCGLGVCYAQRKGYF---SKETSFQKSNSSSKATTMSENVQWL
jam 295 TSSFLV
35638 293 TPVIPALWKAAAGGSRGQEF

Figure 17

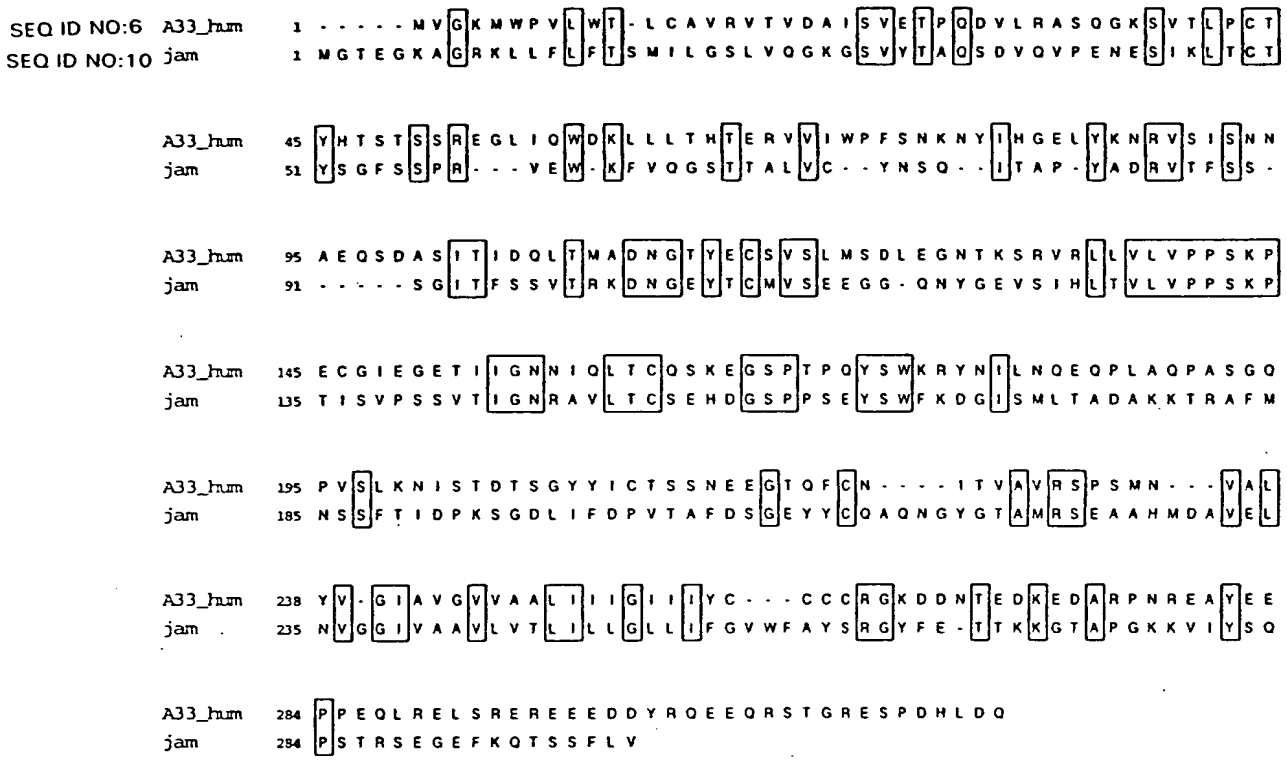


Figure 18

cDNA hybridization of A33 homolog 40628 to human tissues

Tissue	Expression
whole brain	+
amygdala	+
caudate nucleus	+
cerebellum	-
cerebral cortex	+
frontal lobe	+
hippocampus	+
medulla oblongata	+
occipital lobe	+
putamen	+
sustantia nigra	+
temporal lobe	+
thalamus	+
nucleus accumbeus	+
spinal cord	-
heart	++
aorta	+
skeletal muscle	+
colon	+++
bladder	++
uterus	+
prostate	+++
stomach	+++
testis	++
ovary	+++
pancreas	++
pituitary gland	++
adrenal gland	++
thyroid gland	++
salivary gland	+++
mammary gland	++
kidney	+++
liver	++
small intestine	++
spleen	++
thymus	++
peripheral leukocyte	+
lymph node	+
bone marrow	+
appendix	+
lung	++++
trachea	++++
placenta	++++
fetal brain	+
fetal heart	+
fetal kidney	++
fetal liver	+++
fetal spleen	+
fetal lung	++++

Figure 19

Elevated mRNA for Murine JAM in CRF2-4 -/- Colitic Mice as Compared to Wildtype Mice

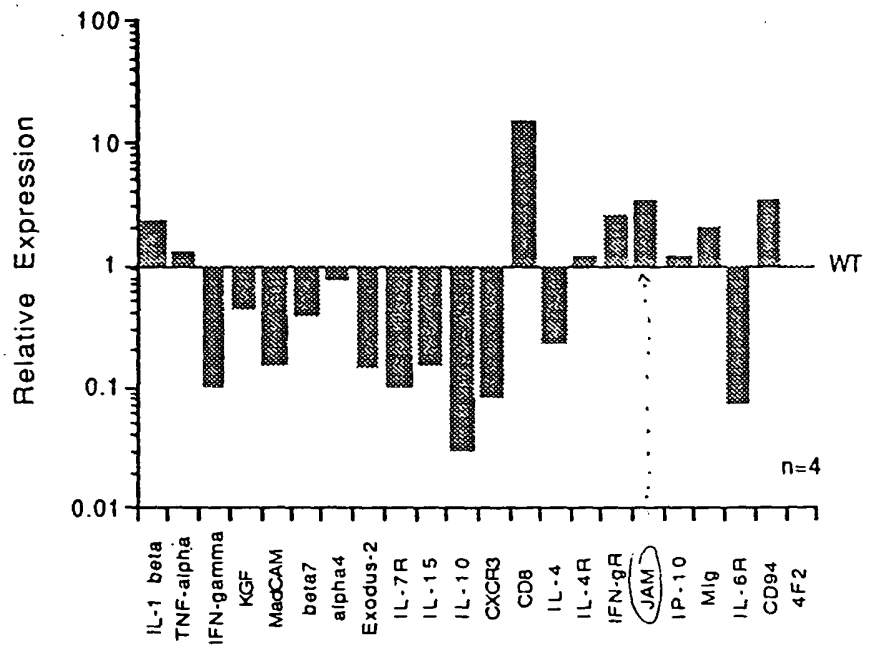


Figure 20

PIN370 Binds to the Cell Surface of Human Neutrophils

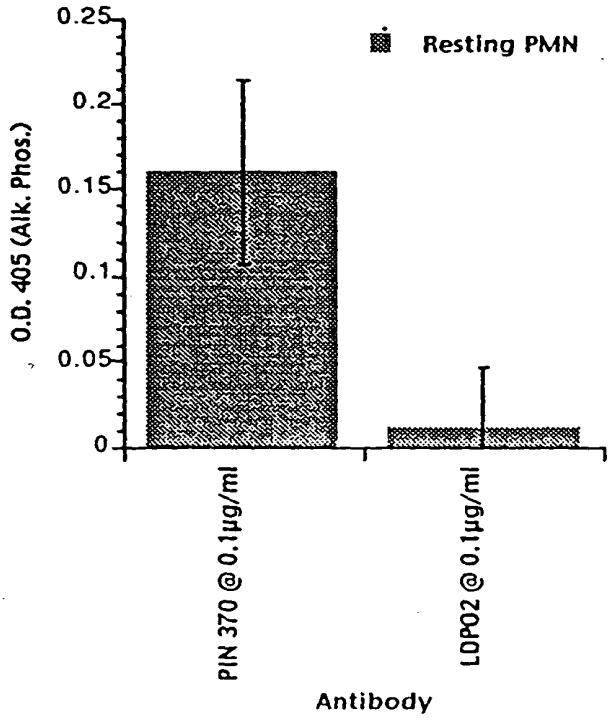


Figure 21

Figure 22

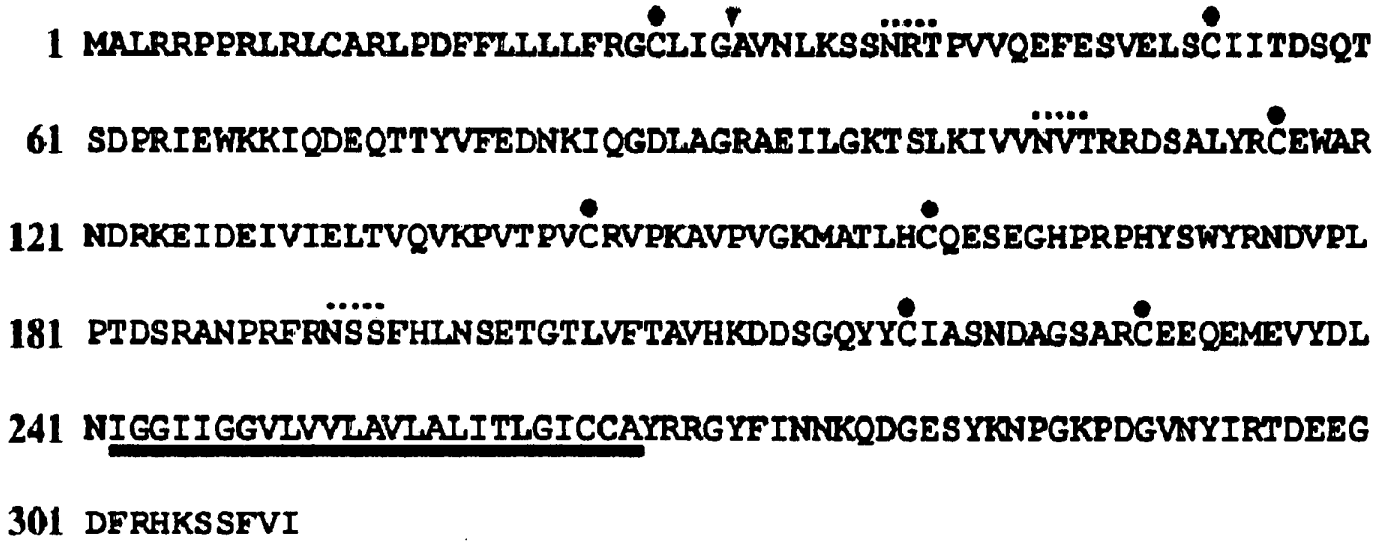

1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT
61 SDPRIEWKKIQDEQTTYVFEDNKIQGDLAGRAEILGKTSLKIVVNVTRRDSALYRCEWAR
121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL
181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL
241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG
301 DFRHKSSFVI

Figure 23

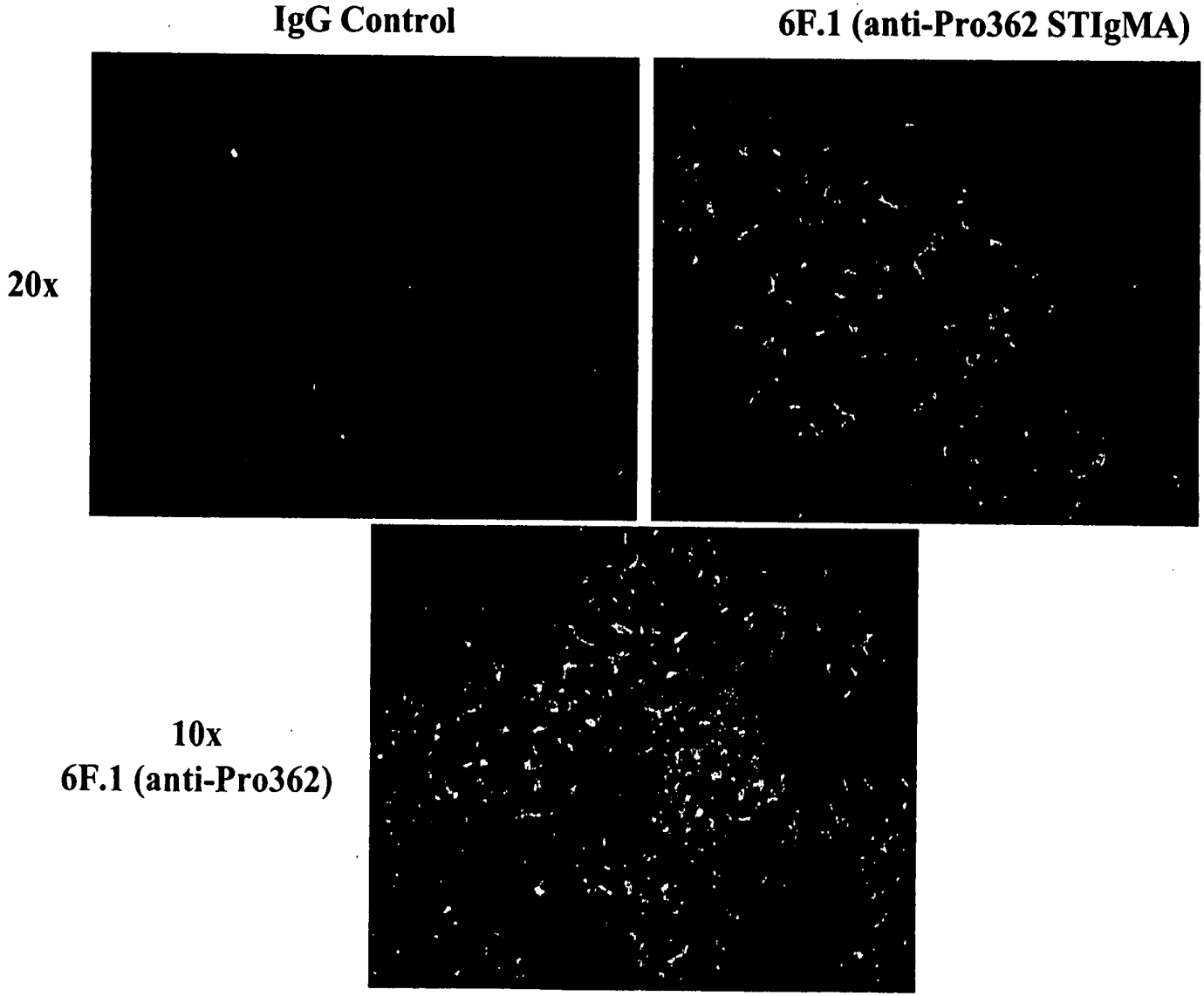


Figure 24

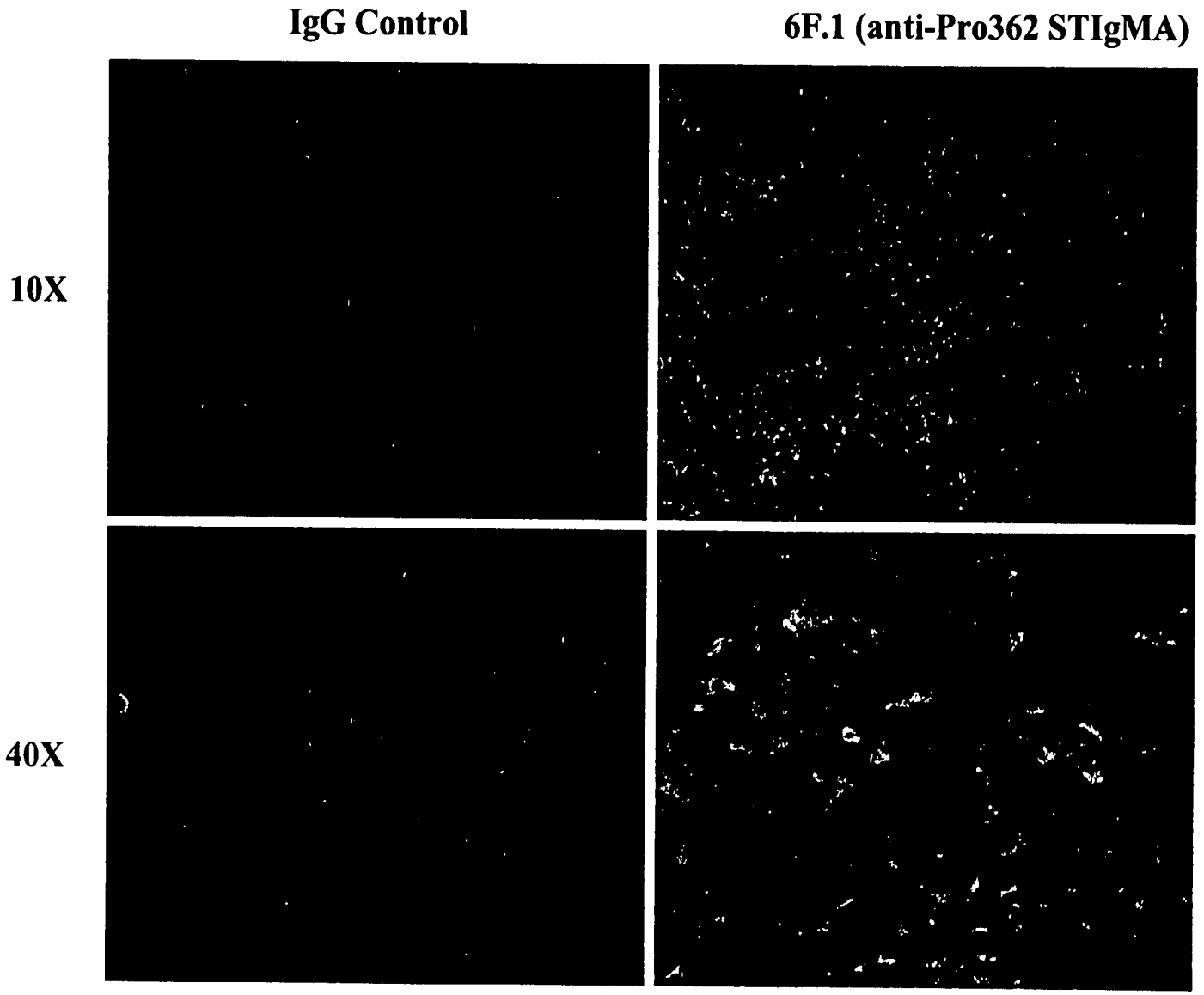
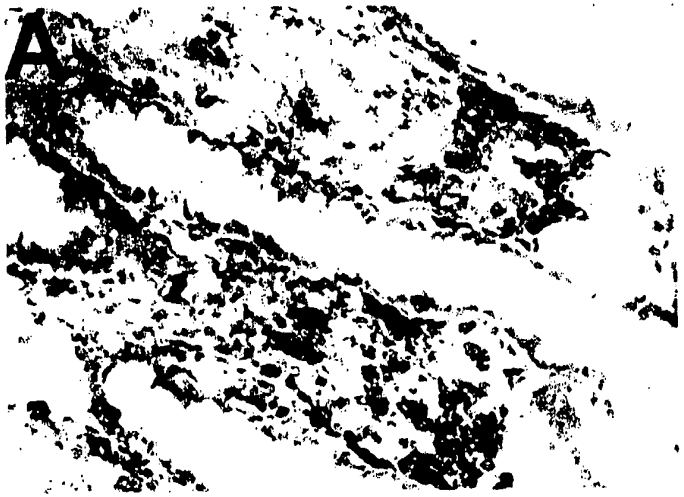
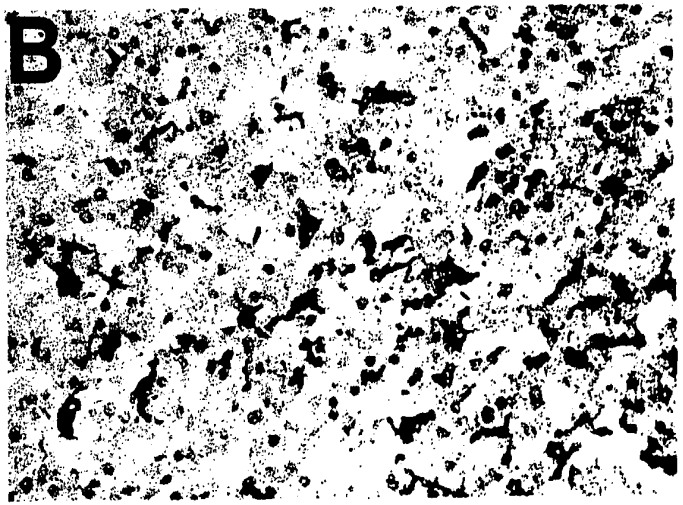


Figure 25

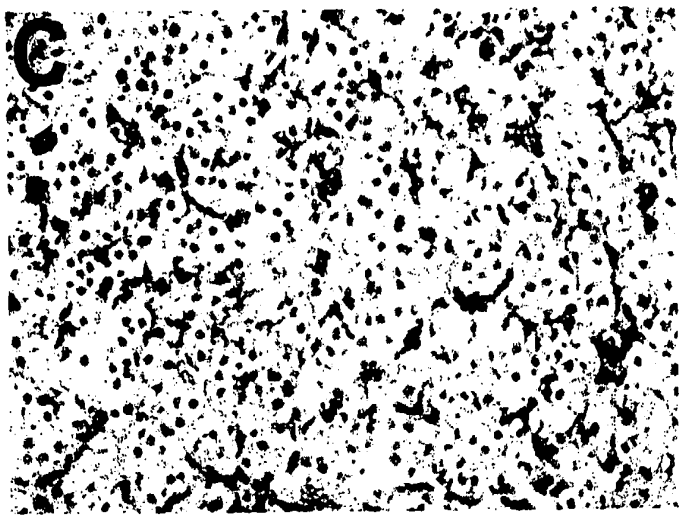
Colon Macs



Kupffer cells



Adrenal Macs



Hofbauer cells

Figure 26

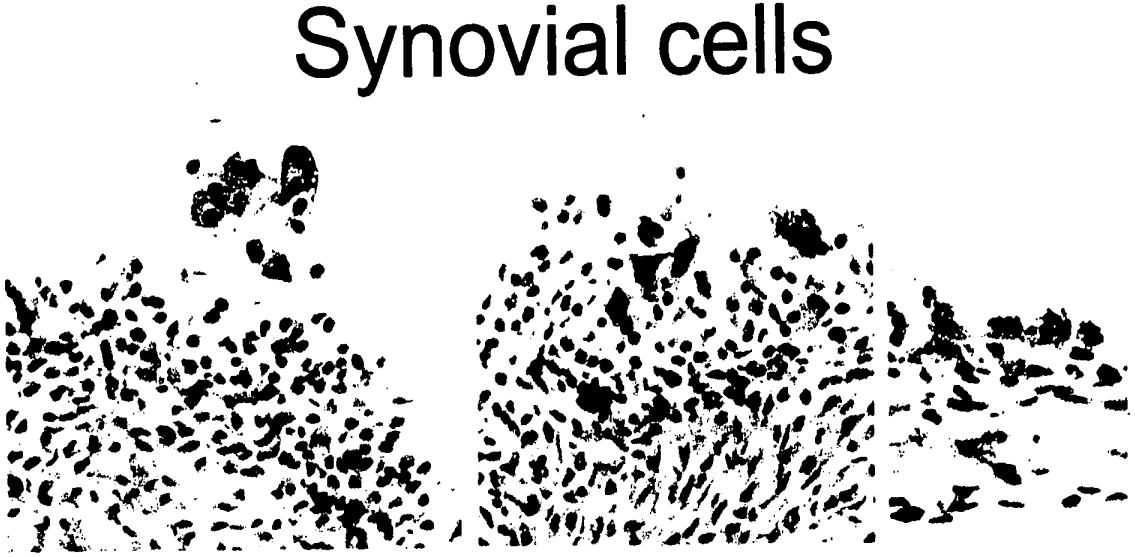


Figure 27

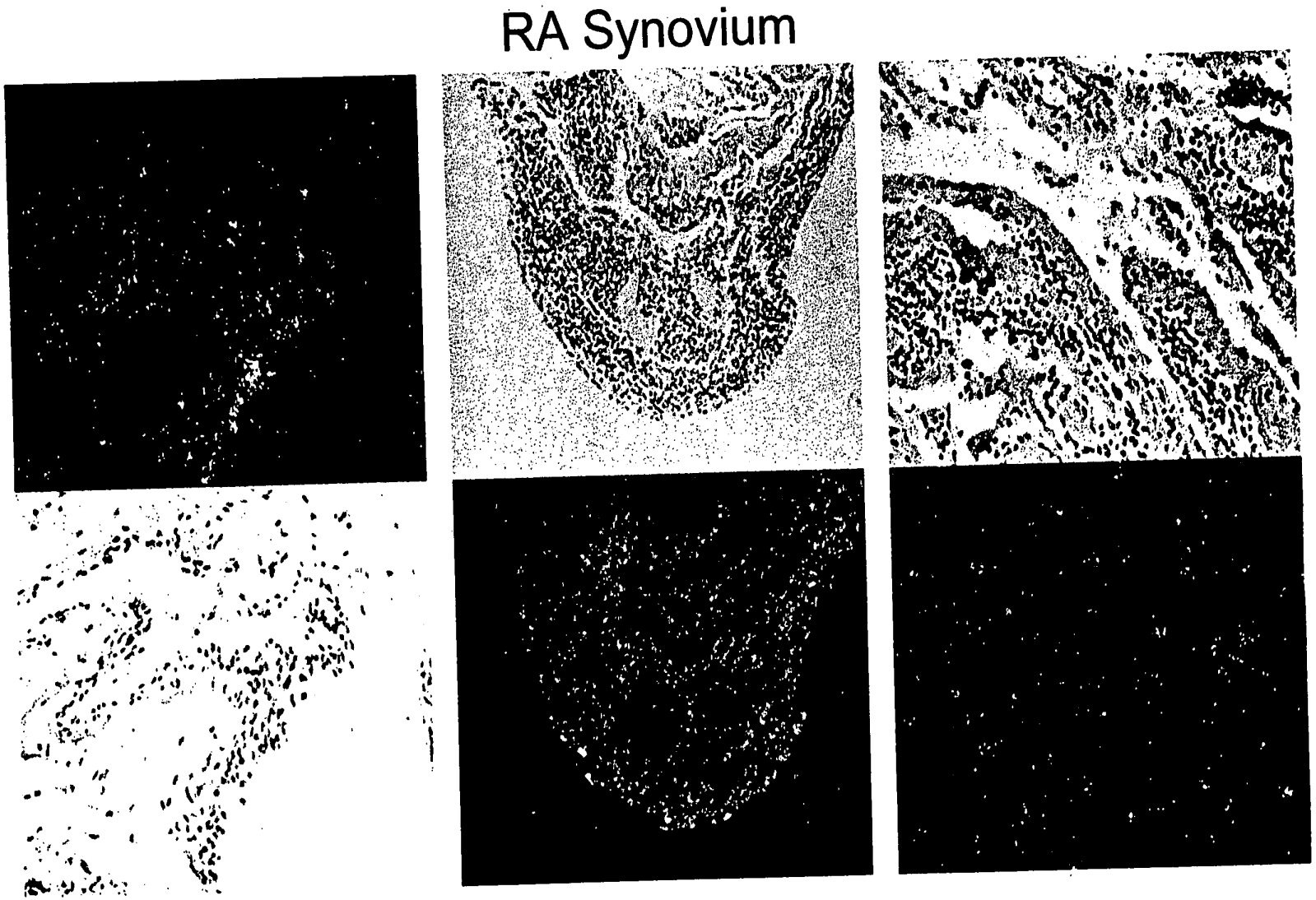


Figure 28

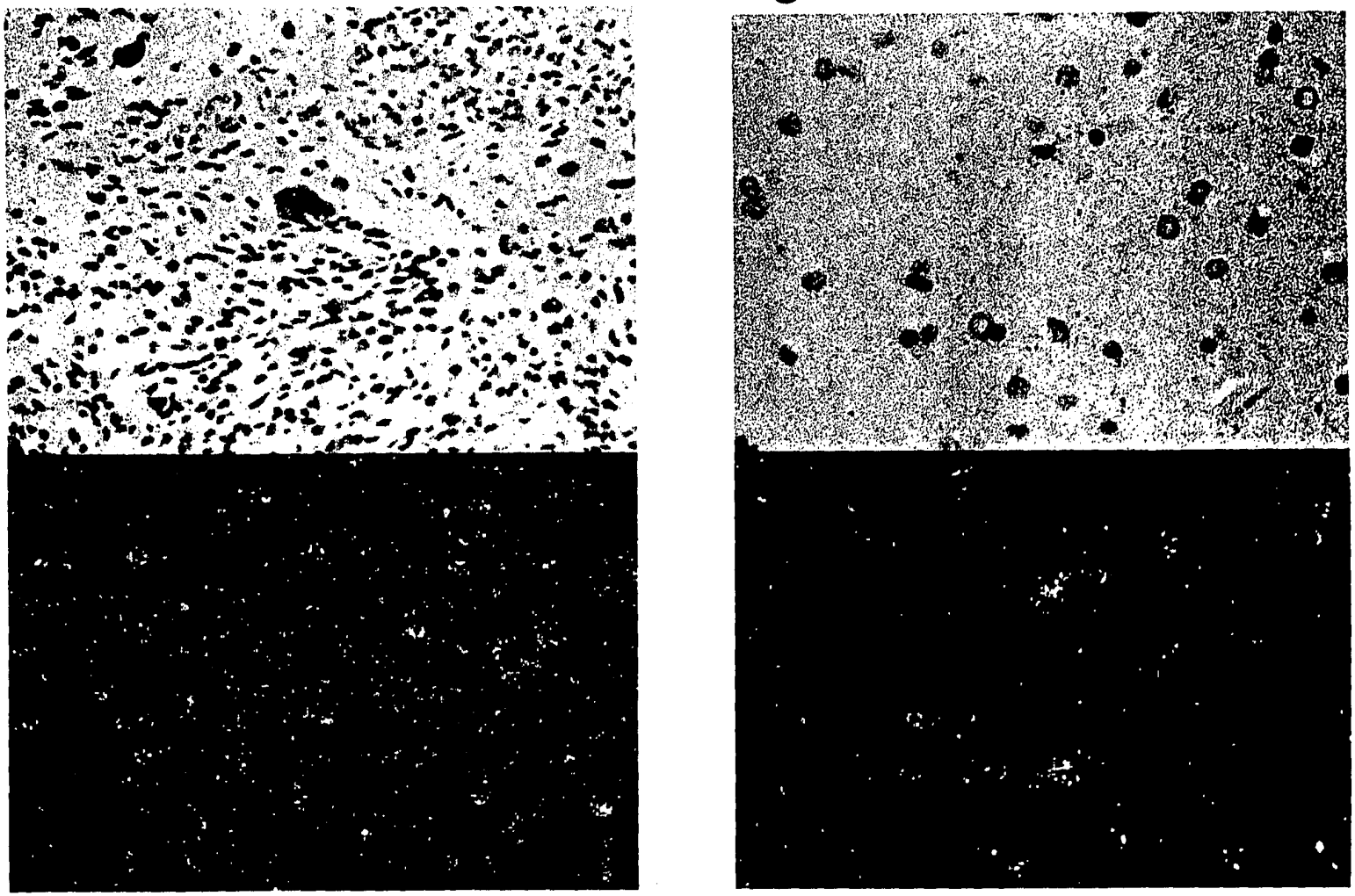


Figure 29

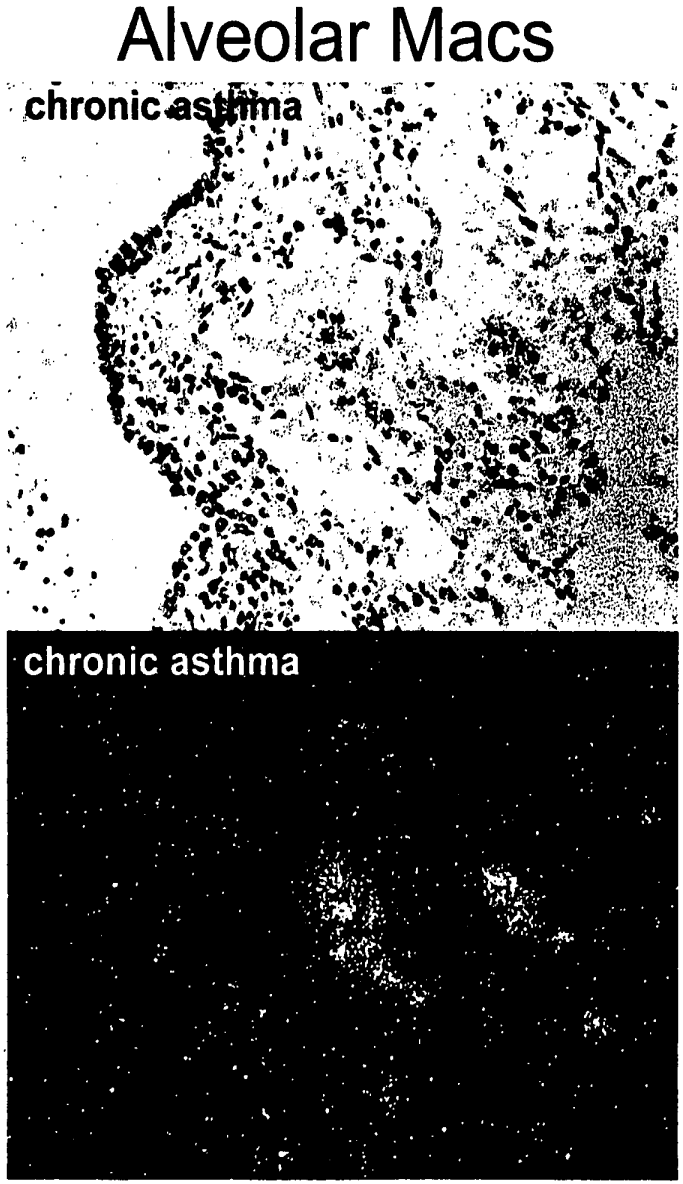


Figure 30

Liver Kupffer cells

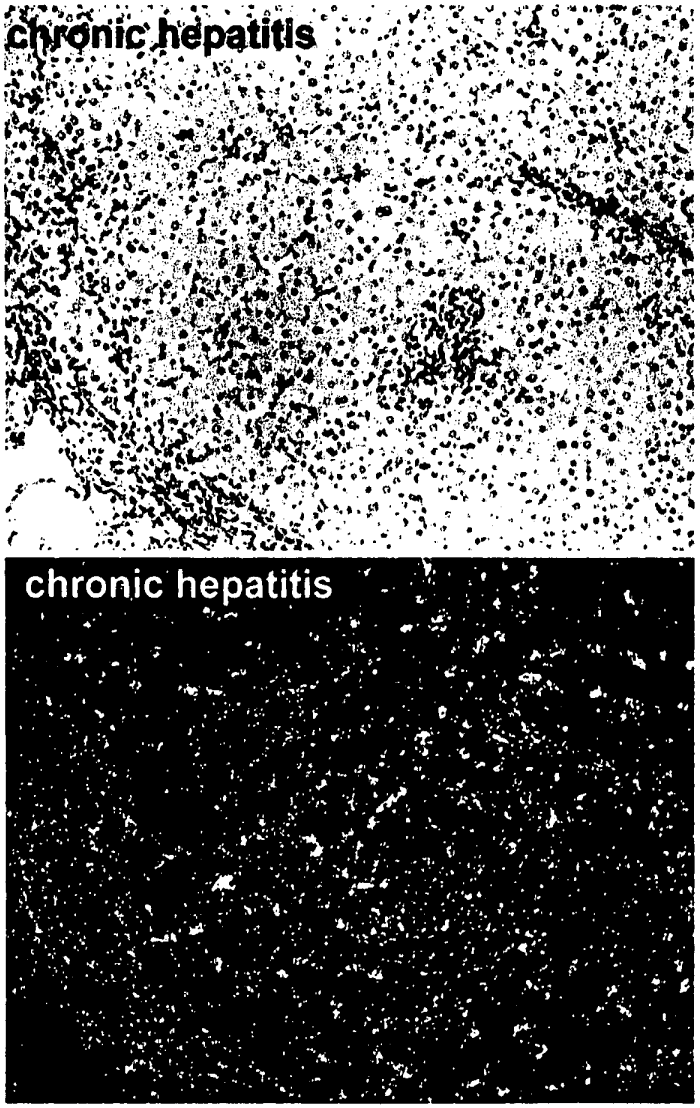


Figure 31

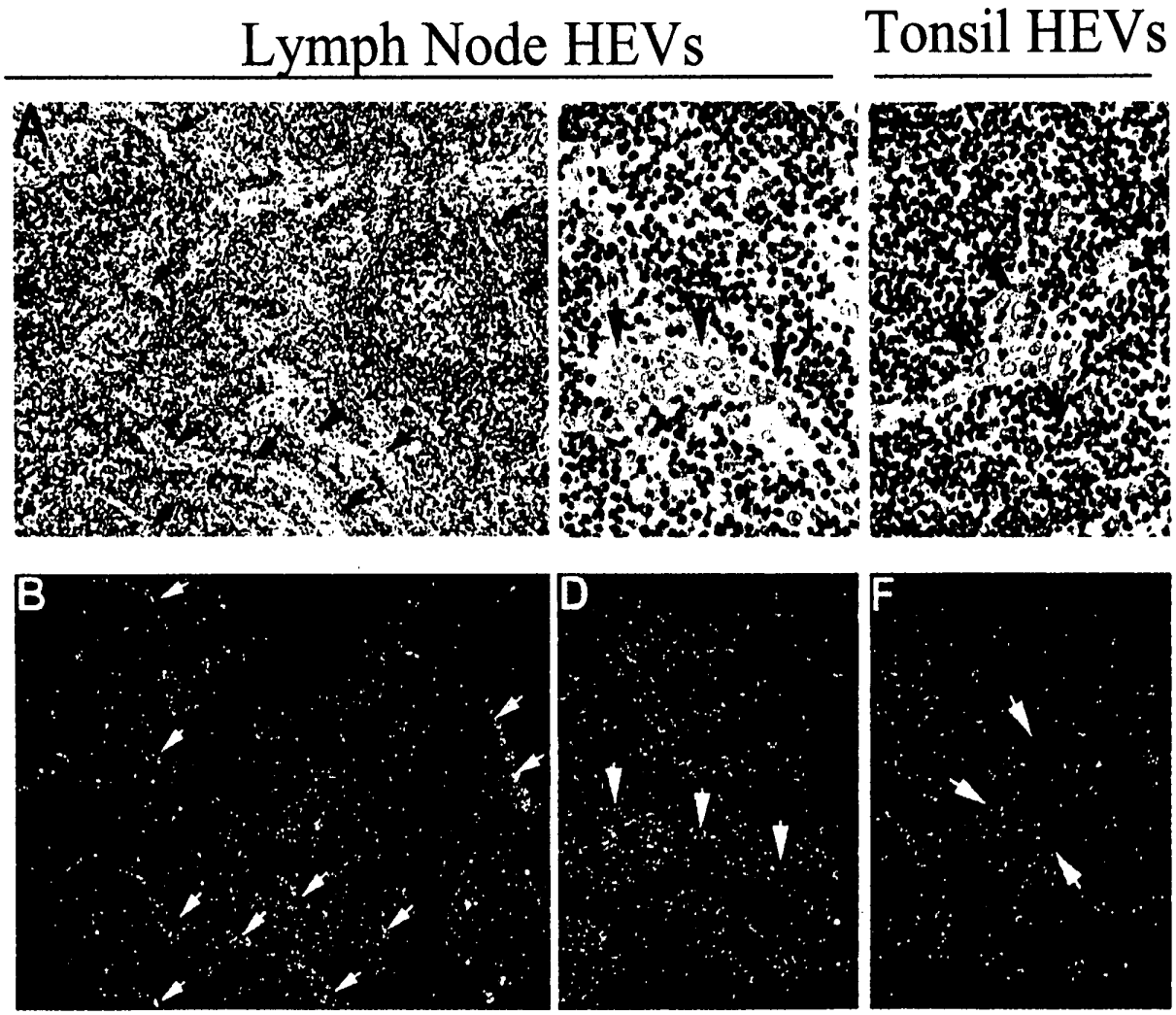


Figure 32

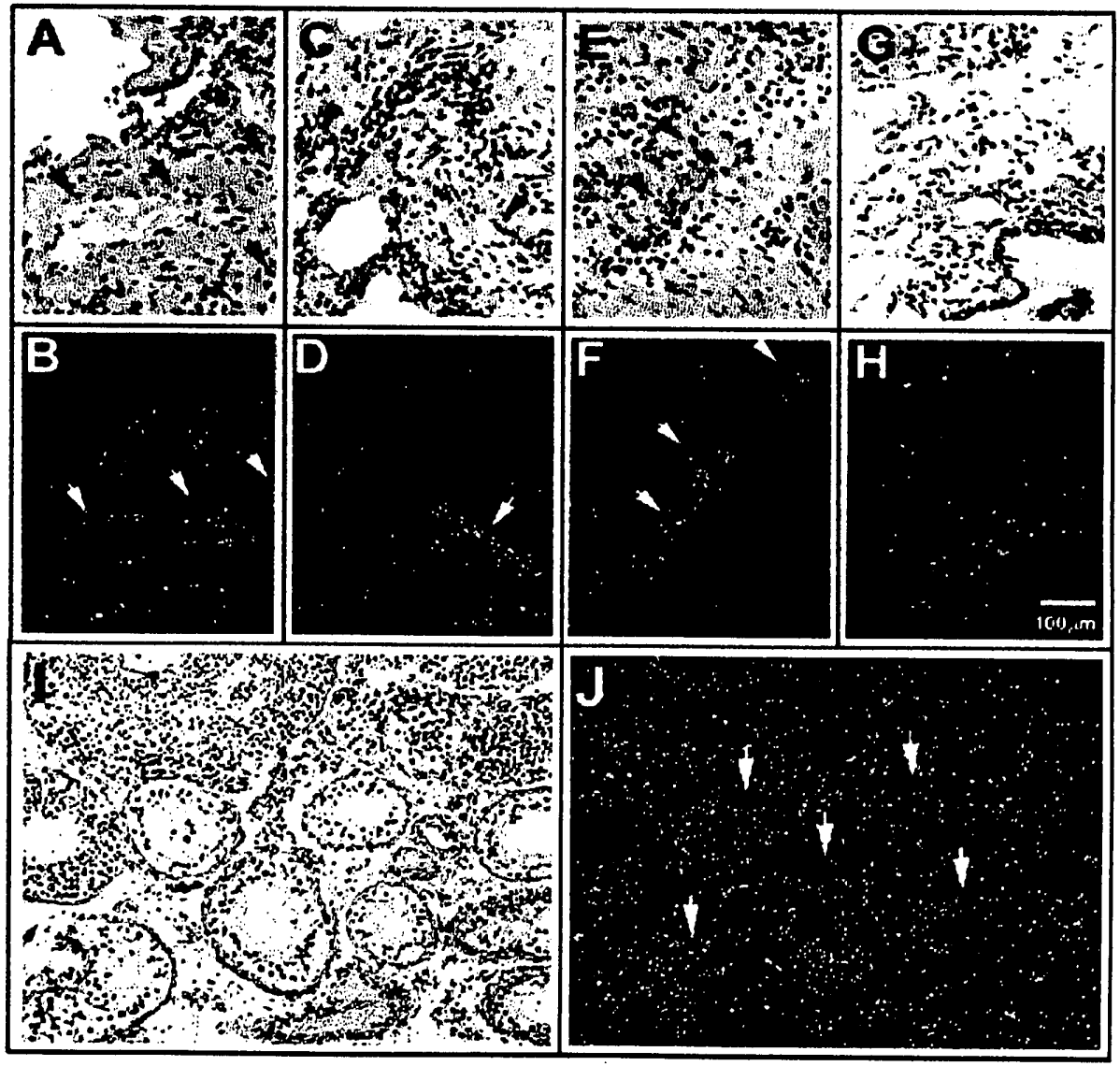


Figure 33

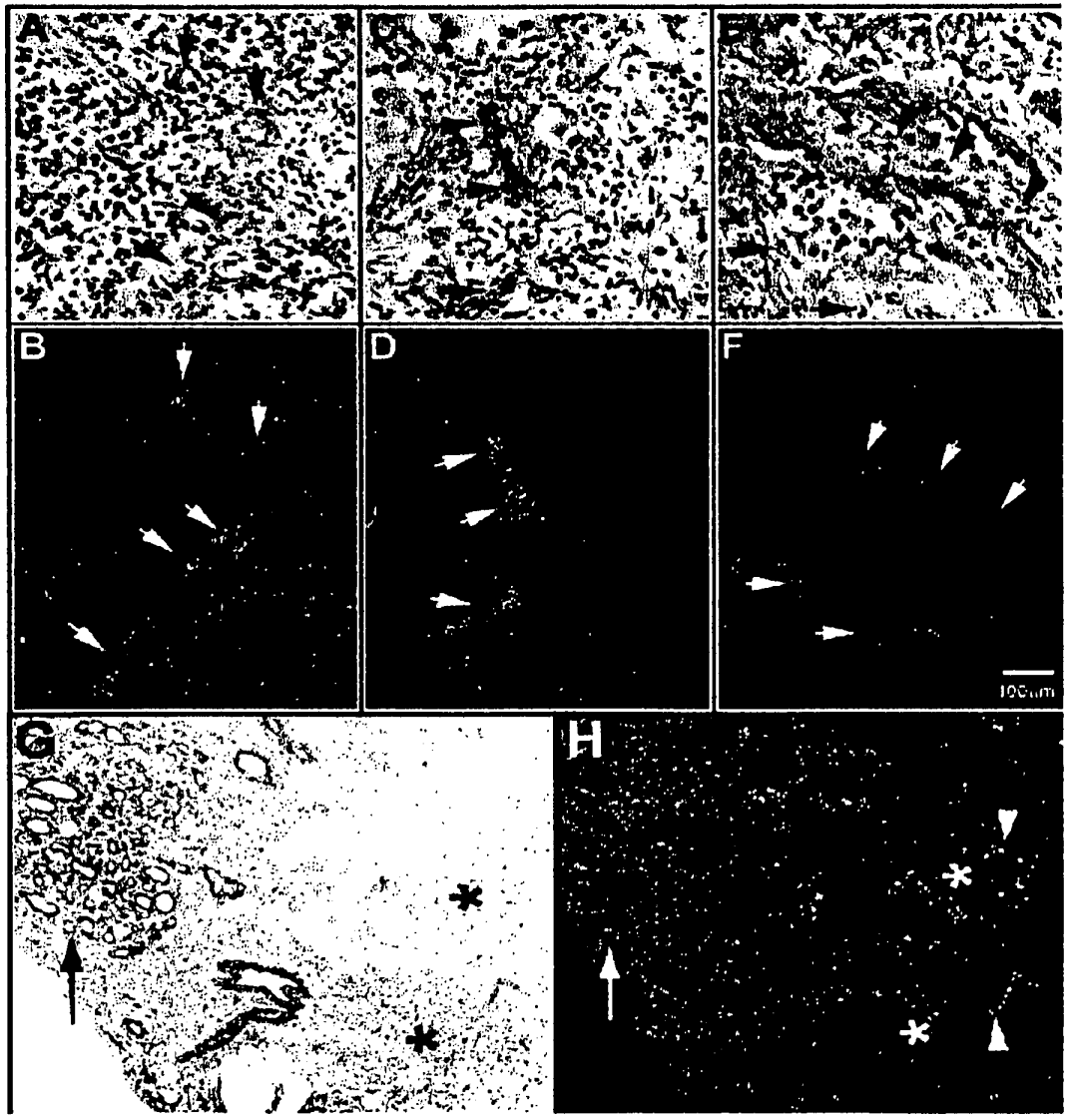
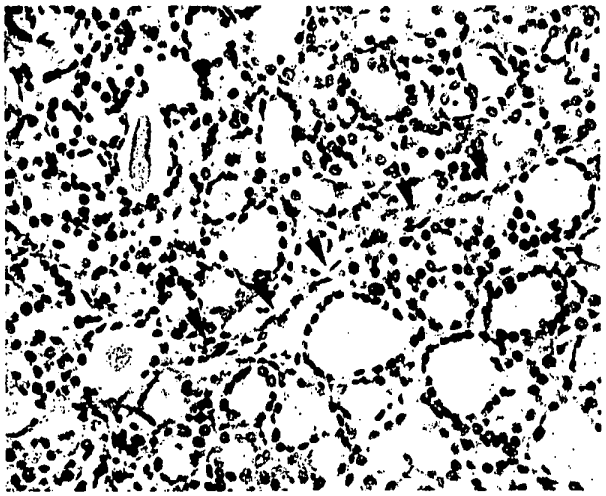


Figure 34



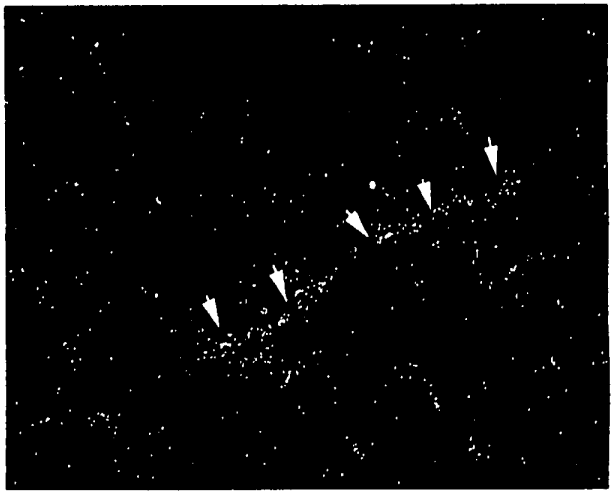


Figure 35

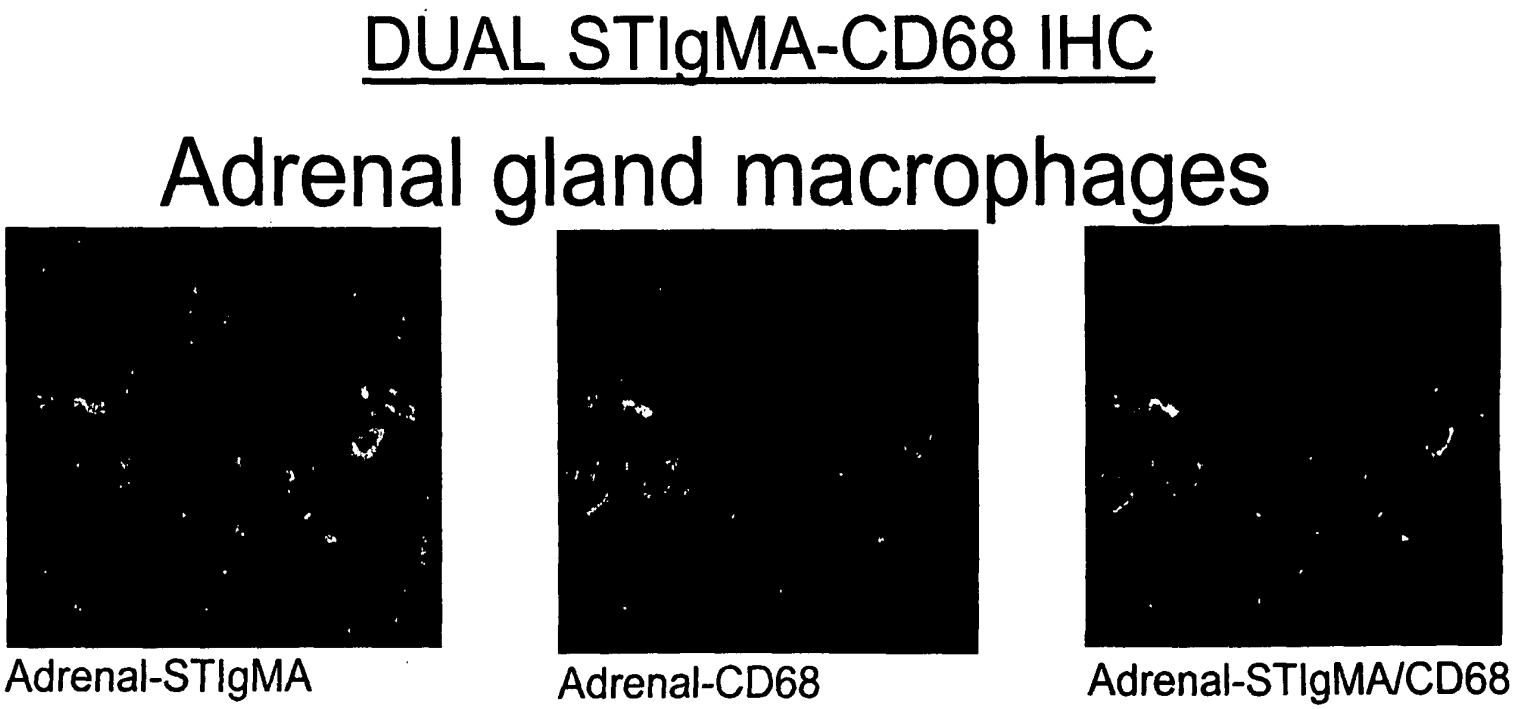
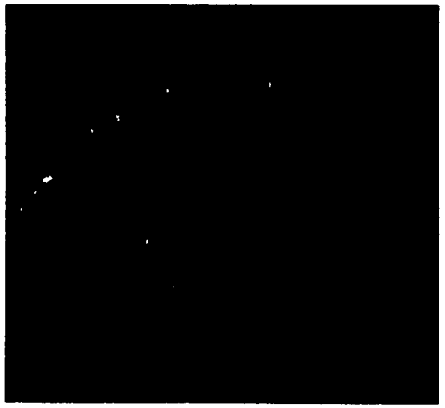

DUAL STIgMA-CD68 IHC
Adrenal gland macrophages
Adrenal-STIgMA
Adrenal-CD68
Adrenal-STIgMA/CD68

Figure 36

Liver Kupffer cells

Liver-STIgMA



Liver-CD68

Figure 37

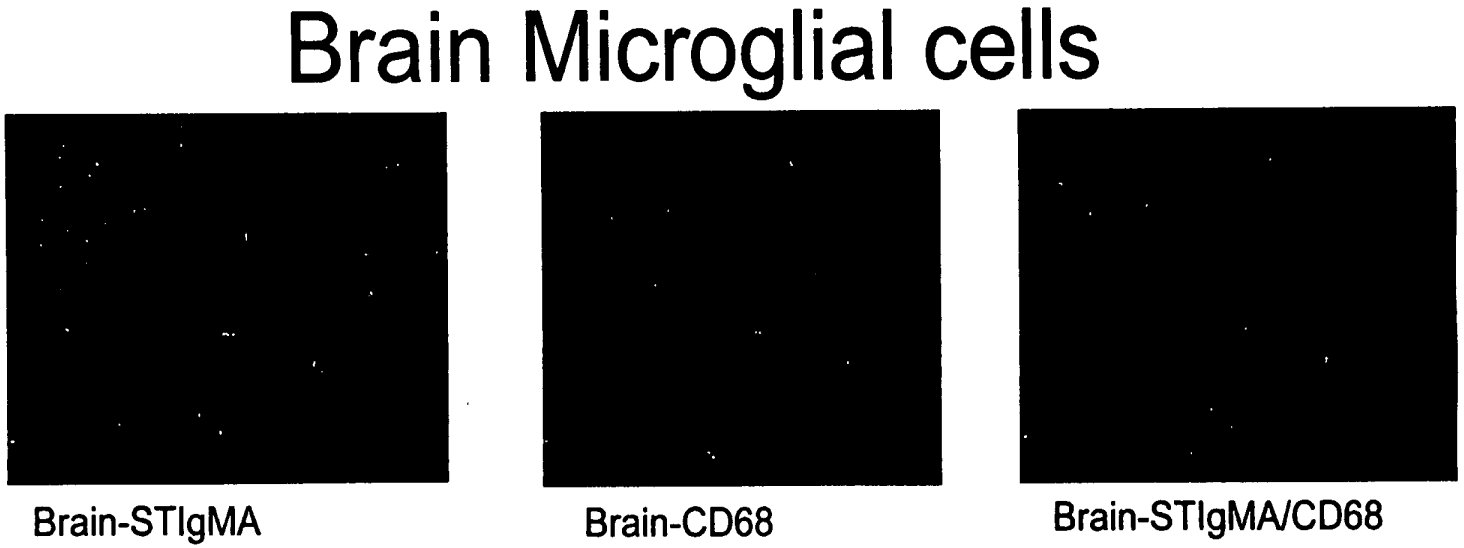
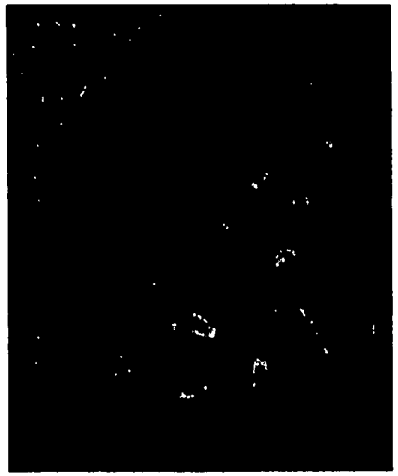
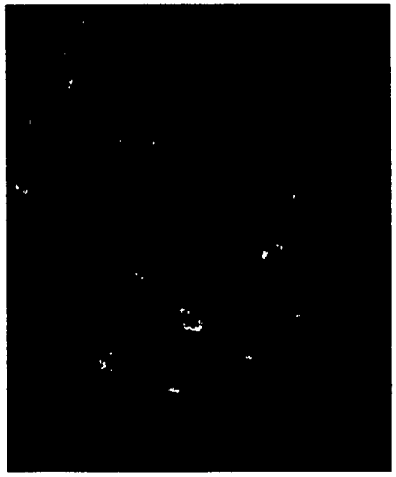

Brain Microglial cells
Brain-STIgMA
Brain-CD68
Brain-STIgMA/CD68

Figure 38

Placental Hofbauer cells



Placenta-STIgMA



Placenta-CD68

Placenta-STIgMA/CD68

Figure 39

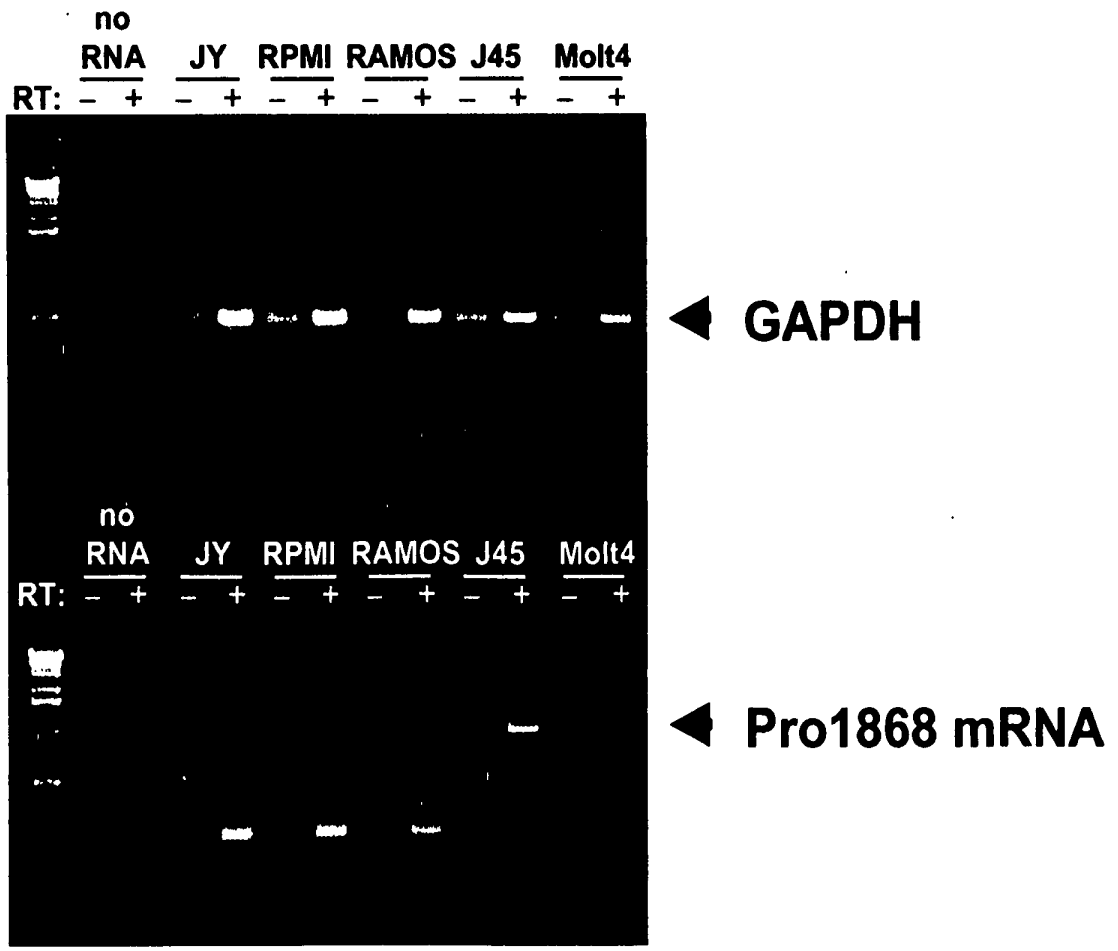

no RNA
JY
RPMI
RAMOS
J45
Molt4
RT: – + – + – + – + – + – +
GAPDH
no RNA
JY
RPMI
RAMOS
J45
Molt4
RT: – + – + – + – + – + – +
Pro1868 mRNA

Figure 40

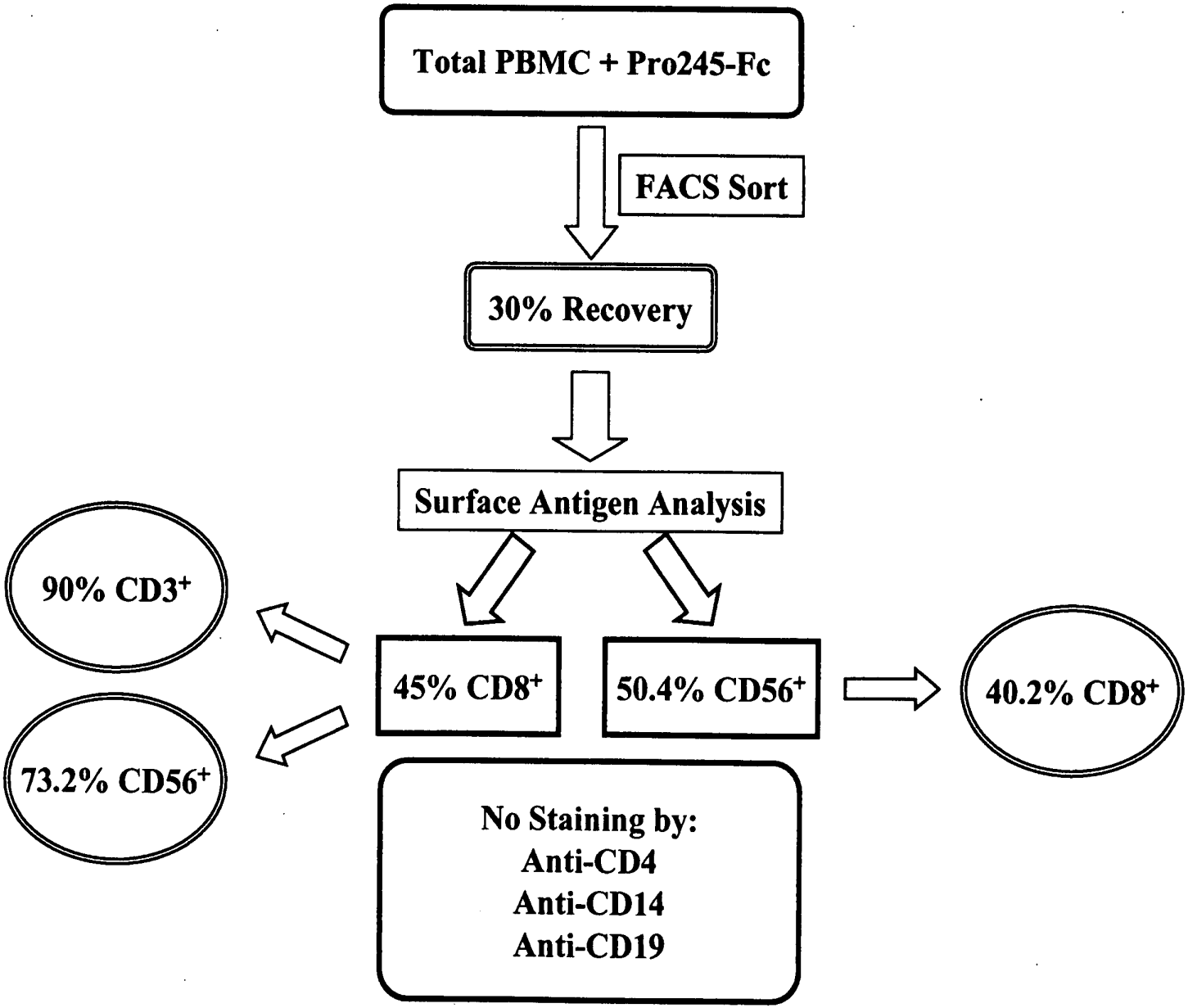
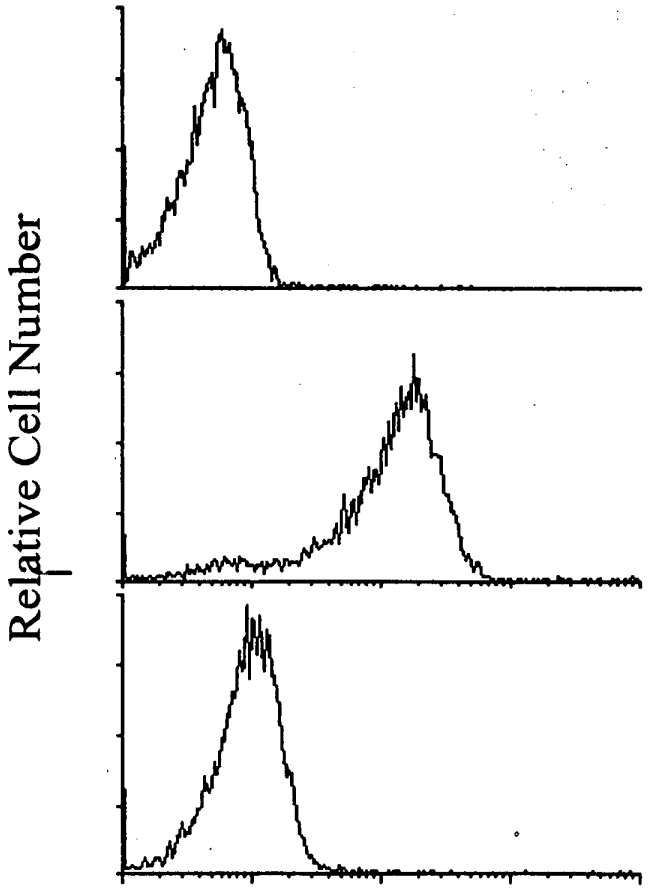

Total PBMC + Pro245-Fc
FACS Sort
30% Recovery
Surface Antigen Analysis
90% CD3+
73.2% CD56+
45% CD8+
50.4% CD56+
40.2% CD8+
No Staining by:
Anti-CD4
Anti-CD14
Anti-CD19

Figure 41



Control Ig

Pro245-Fc (0.2 μg)

Pro245-Fc (0.2 μg)
+
2F9 anti-Pro245 (20 μg)

Figure 42

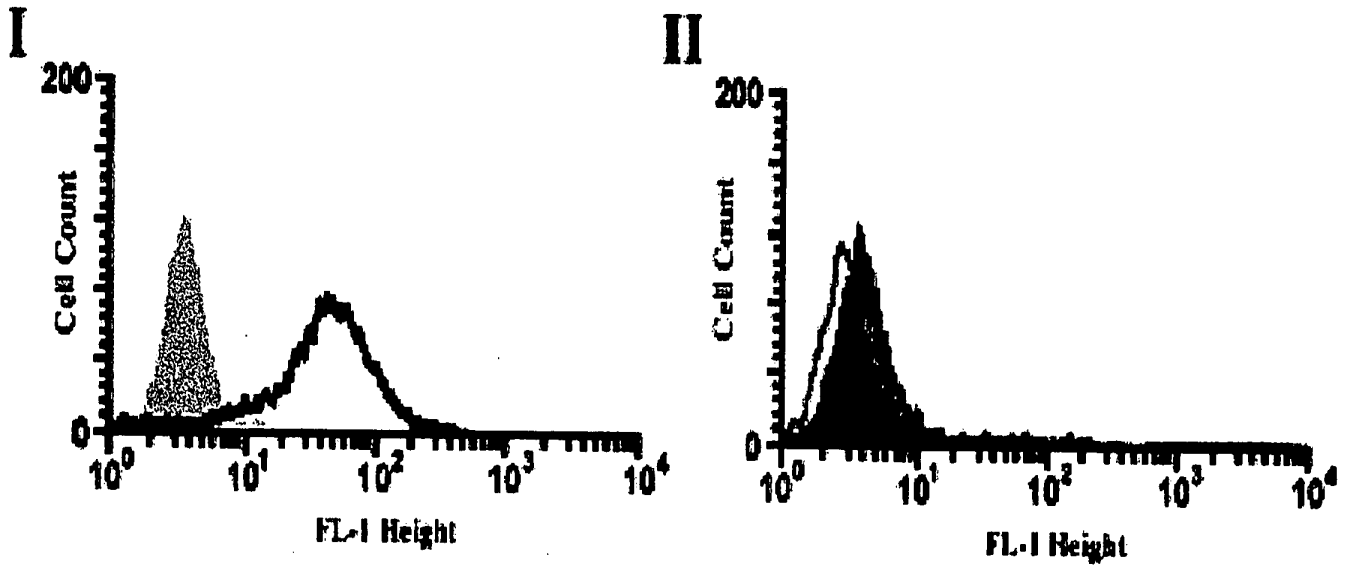

I
200
Cell Count
0
10^0
10^1
10^2
10^3
10^4
FL-1 Height
II
200
Cell Count
0
10^0
10^1
10^2
10^3
10^4
FL-1 Height

Figure 43

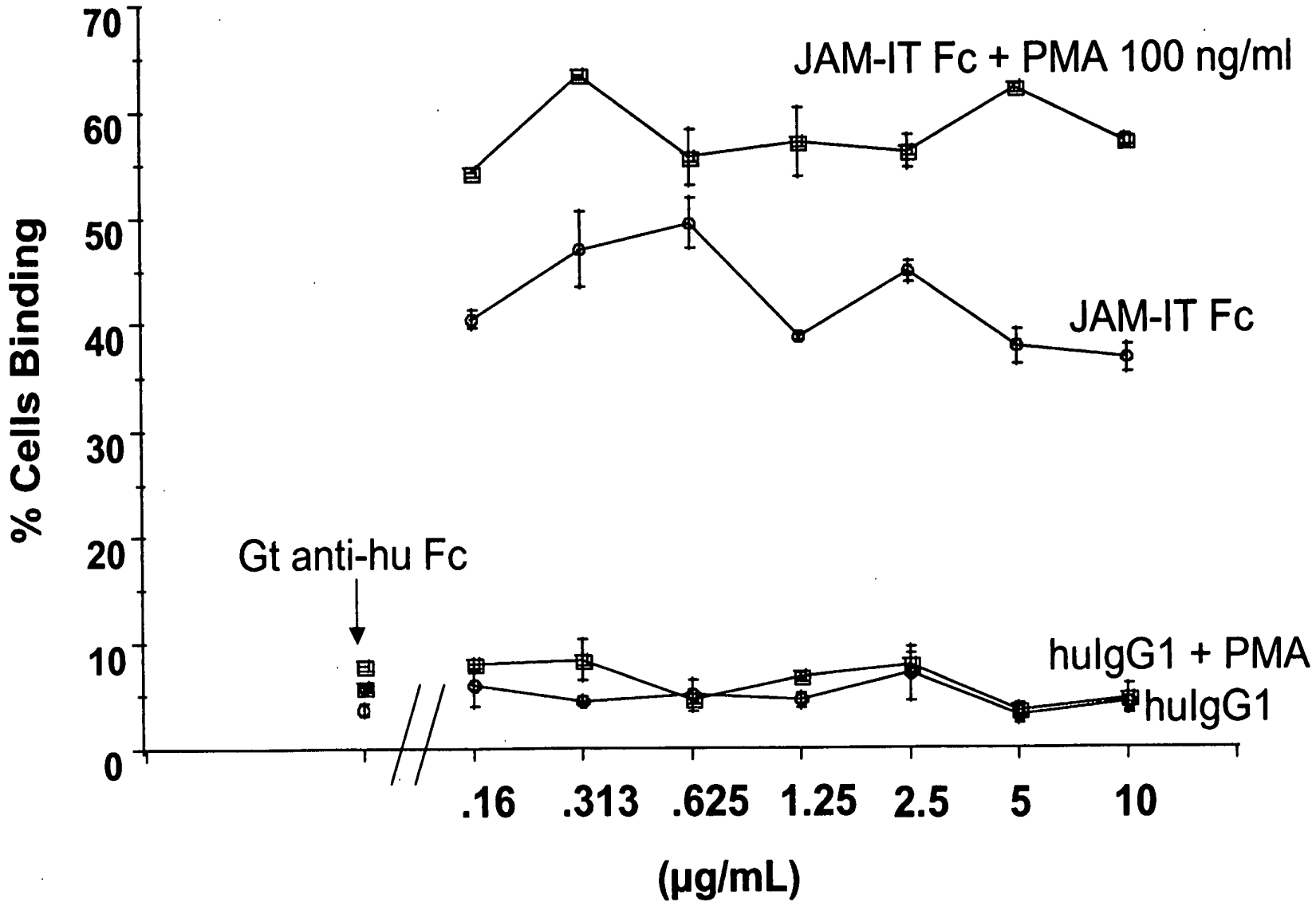

70
60
50
40
30
20
10
0
% Cells Binding
JAM-IT Fc + PMA 100 ng/ml
JAM-IT Fc
Gt anti-hu Fc
huIgG1 + PMA
huIgG1
.16
.313
.625
1.25
2.5
5
10
(µg/mL)

Figure 44

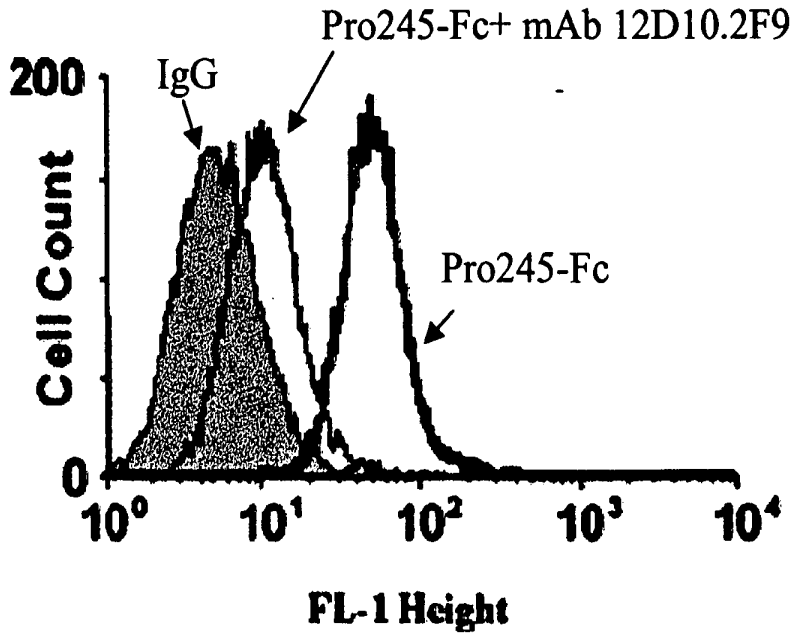

Pro245-Fc+ mAb 12D10.2F9
IgG
Pro245-Fc
200
0
Cell Count
10⁰
10¹
10²
10³
10⁴
FL-1 Height

Figure 45

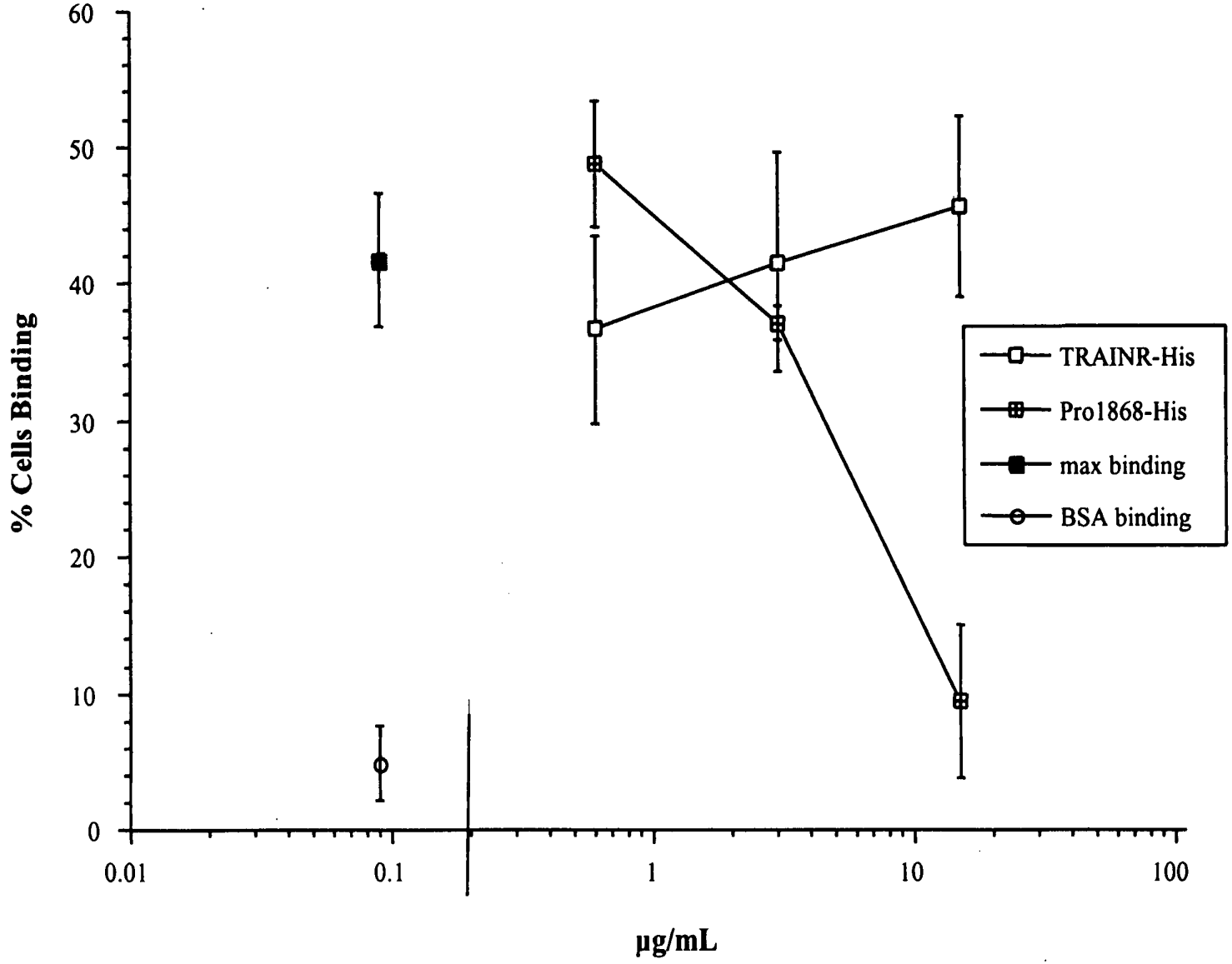
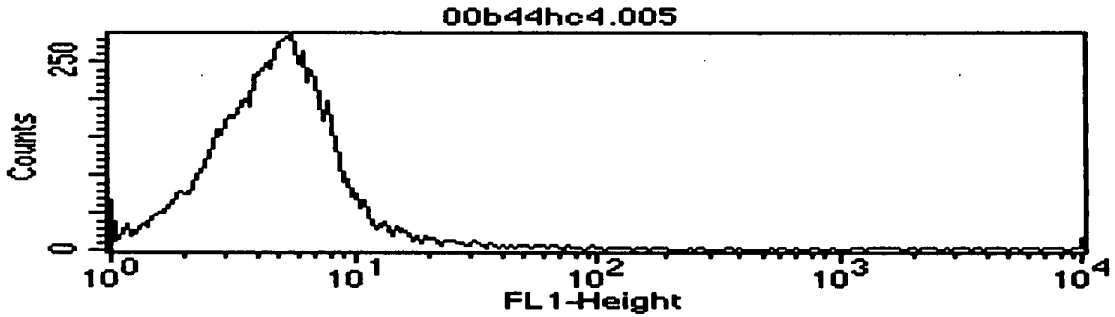
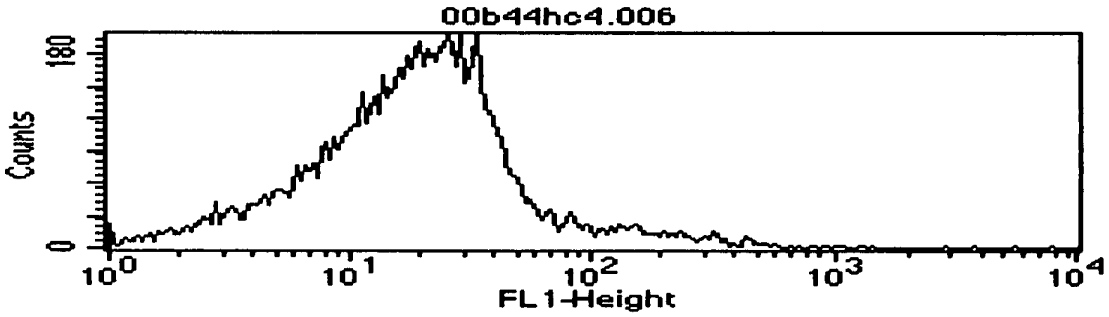

60
50
40
30
20
10
0
% Cells Binding
0.01
0.1
1
10
100
µg/mL
TRAINR-His
Pro1868-His
max binding
BSA binding

Figure 46

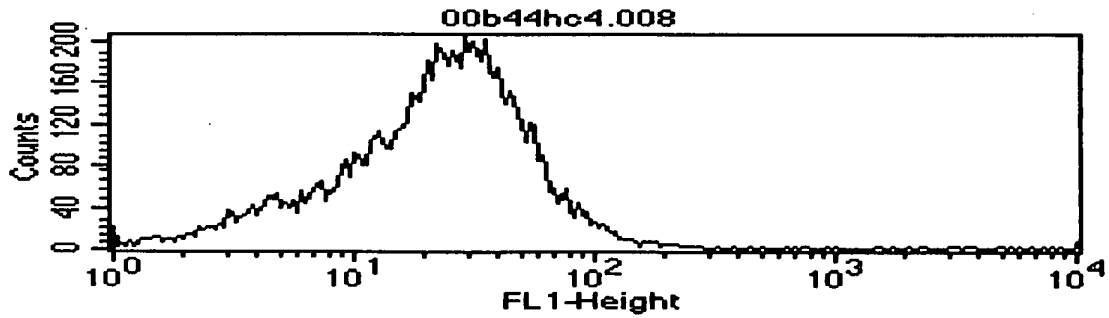
huIgG1



Pro245-Fc (0.2 µg)



Pro245-Fc (0.2 µg)
+
TRAINR-His (10µg)



Pro245-Fc (0.2 µg)
+
Pro1868-His (10µg)

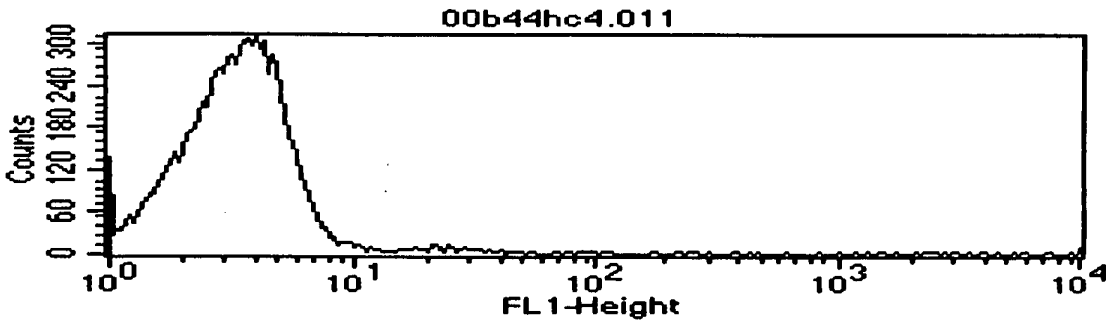


Figure 47

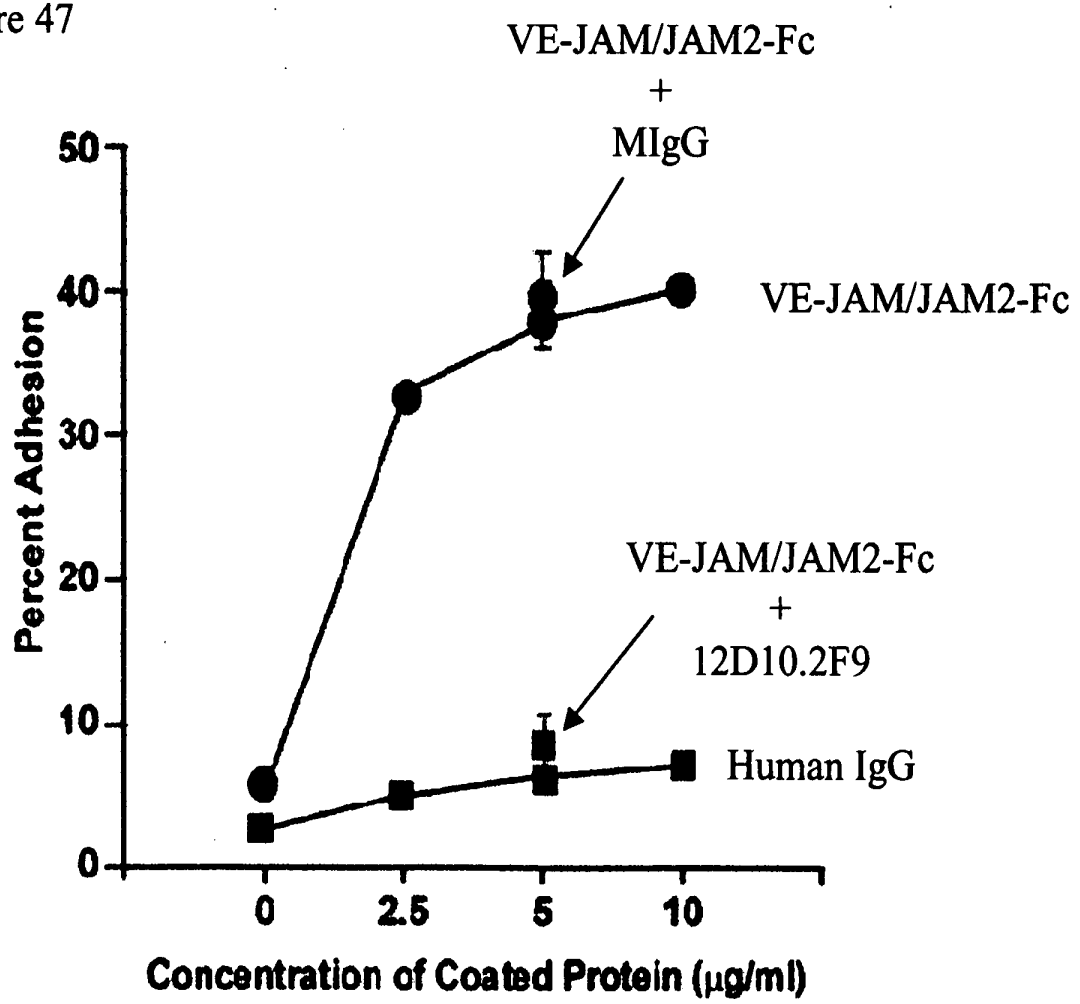

VE-JAM/JAM2-Fc
+
MIgG
VE-JAM/JAM2-Fc
VE-JAM/JAM2-Fc
+
12D10.2F9
Human IgG
Percent Adhesion
50
40
30
20
10
0
0
2.5
5
10
Concentration of Coated Protein (µg/ml)

Figure 48

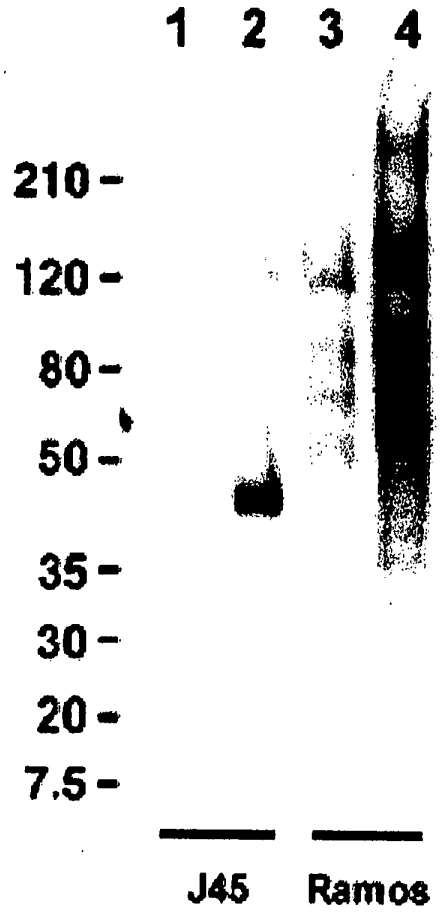


Figure 49

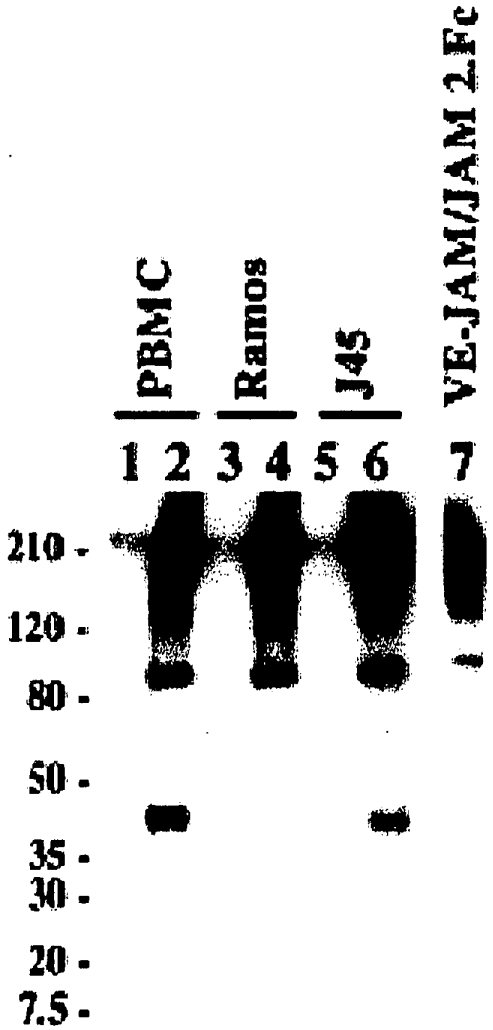


Figure 50

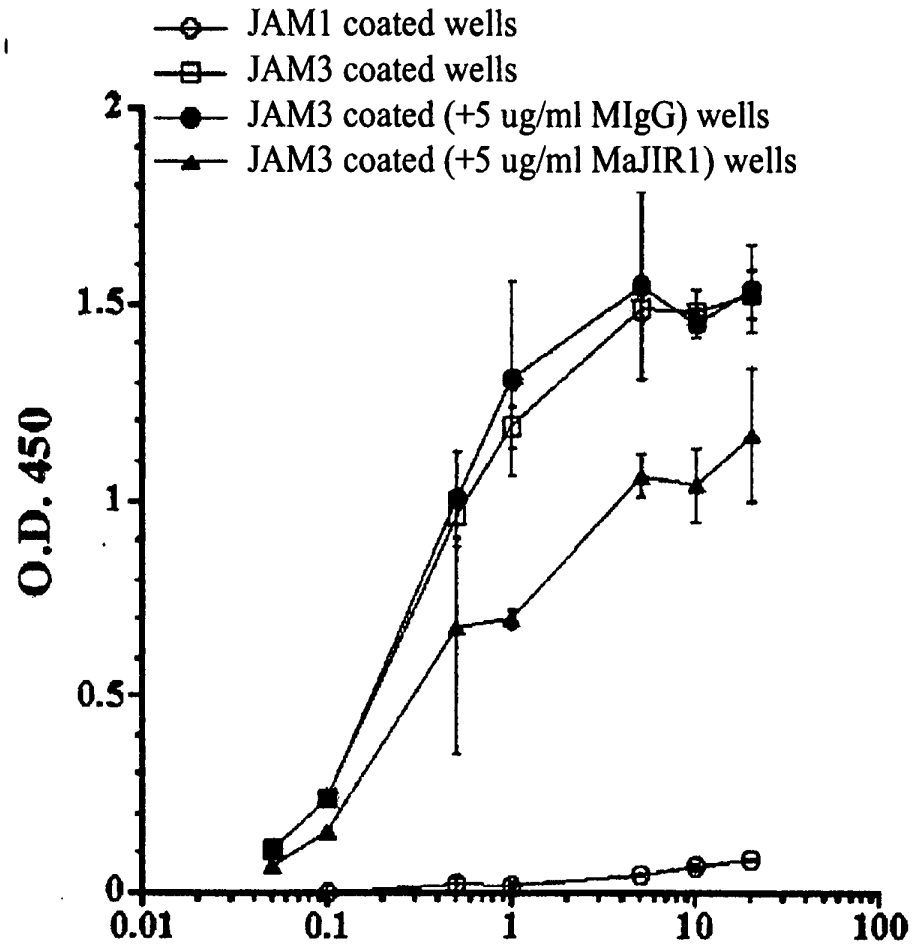

JAM1 coated wells
JAM3 coated wells
JAM3 coated (+5 ug/ml MIgG) wells
JAM3 coated (+5 ug/ml MaJIR1) wells
O.D. 450
2
1.5
1
0.5
0
0.01
0.1
1
10
100
[JAM2-Fc-Biotin]

Figure 51

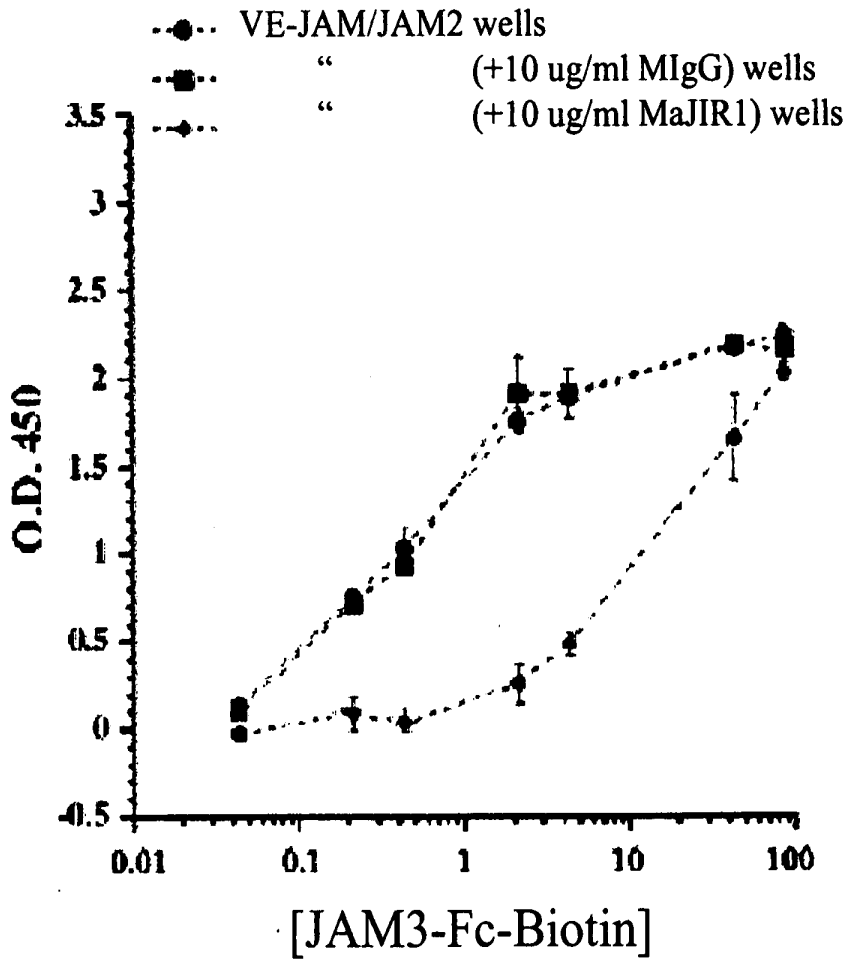

VE-JAM/JAM2 wells
" (+10 ug/ml MIgG) wells
" (+10 ug/ml MaJIR1) wells
O.D. 450
3.5
3
2.5
2
1.5
1
0.5
0
-0.5
0.01
0.1
1
10
100
[JAM3-Fc-Biotin]

Figure 52

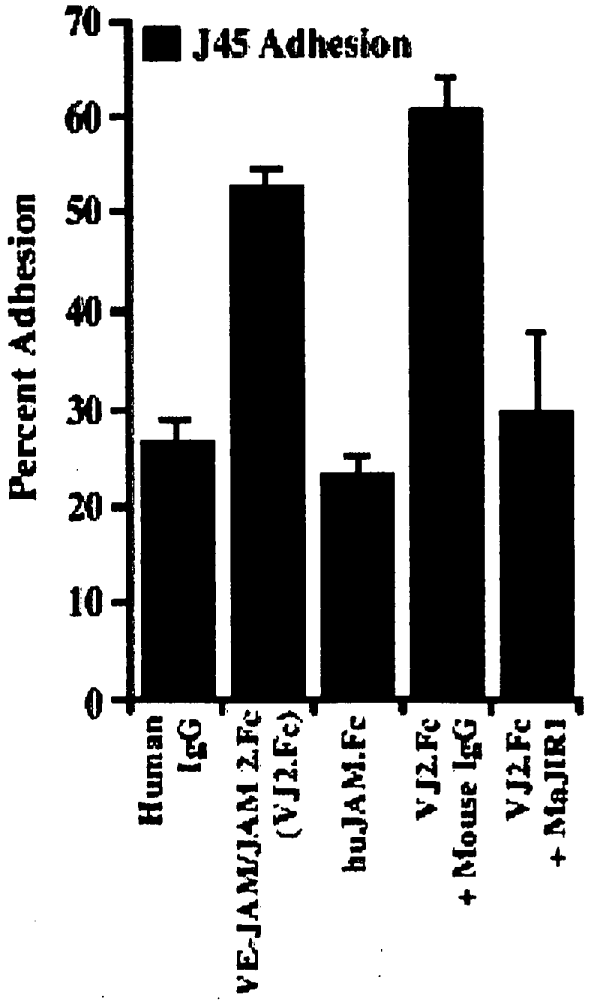

J45 Adhesion
Percent Adhesion
70
60
50
40
30
20
10
0
Human IgG
VE-JAM/JAM 2.Fc (VJ2.Fc)
huJAM.Fc
VJ2.Fc + Mouse IgG
VJ2.Fc + MaJIR1

Figure 53

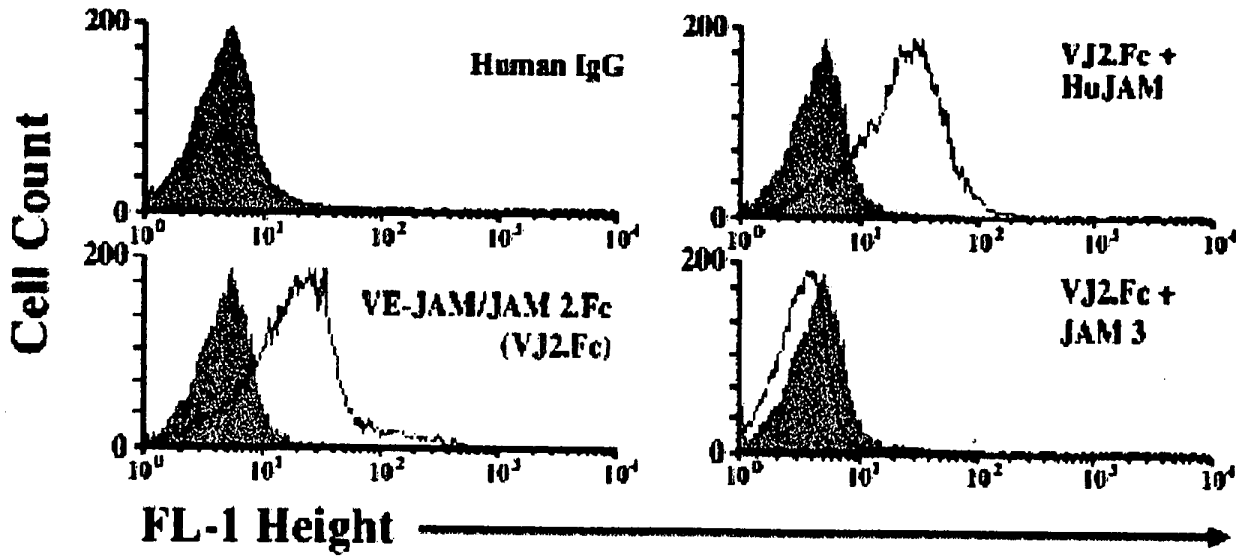

Cell Count
200
0
Human IgG
VE-JAM/JAM 2.Fc
(VJ2.Fc)
VJ2.Fc +
HuJAM
VJ2.Fc +
JAM 3
FL-1 Height

Figure 54

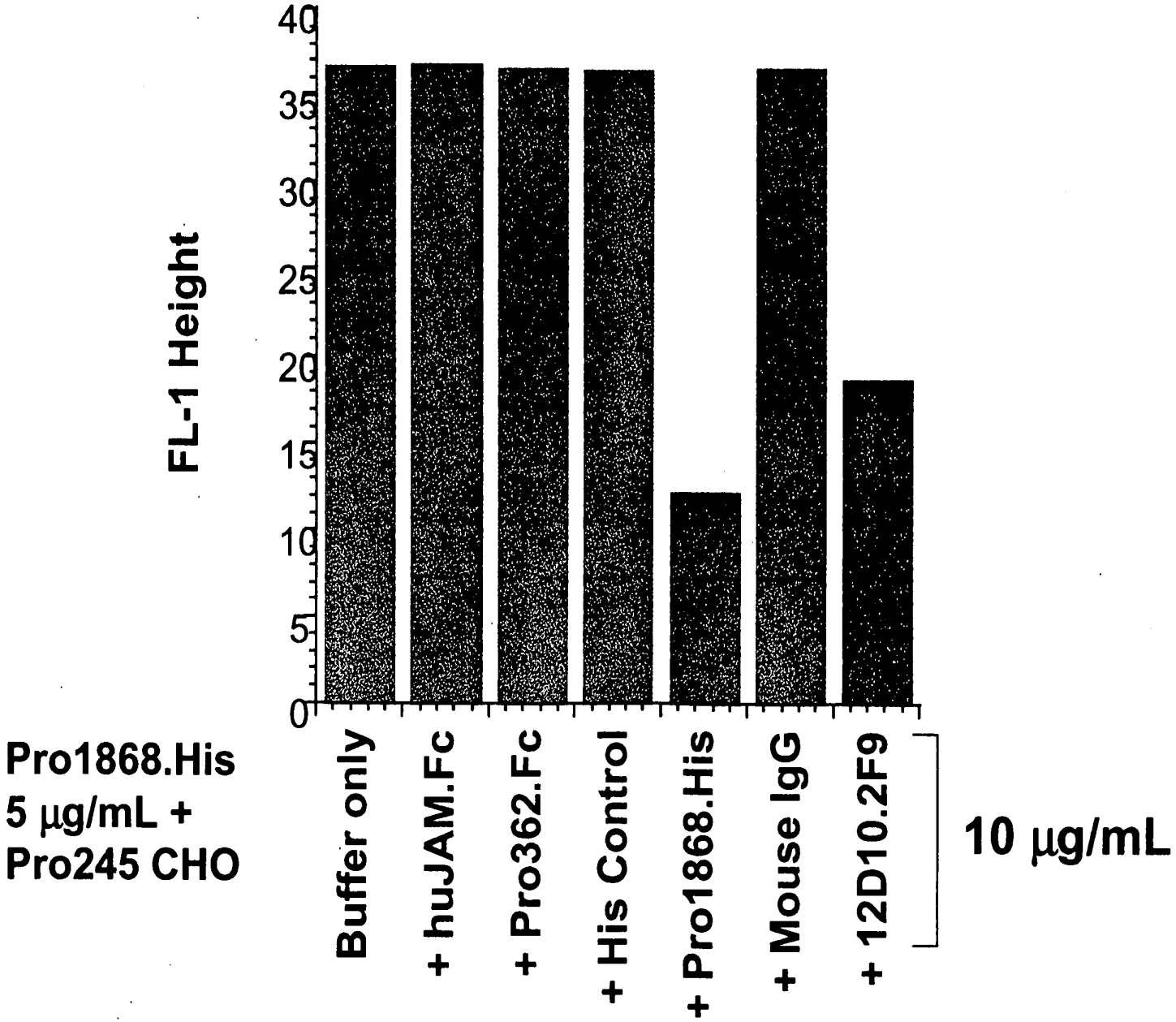
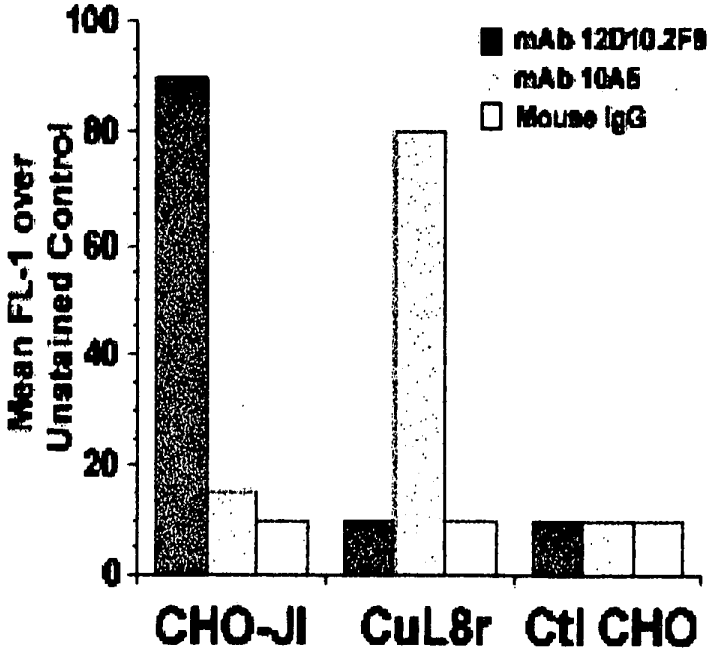
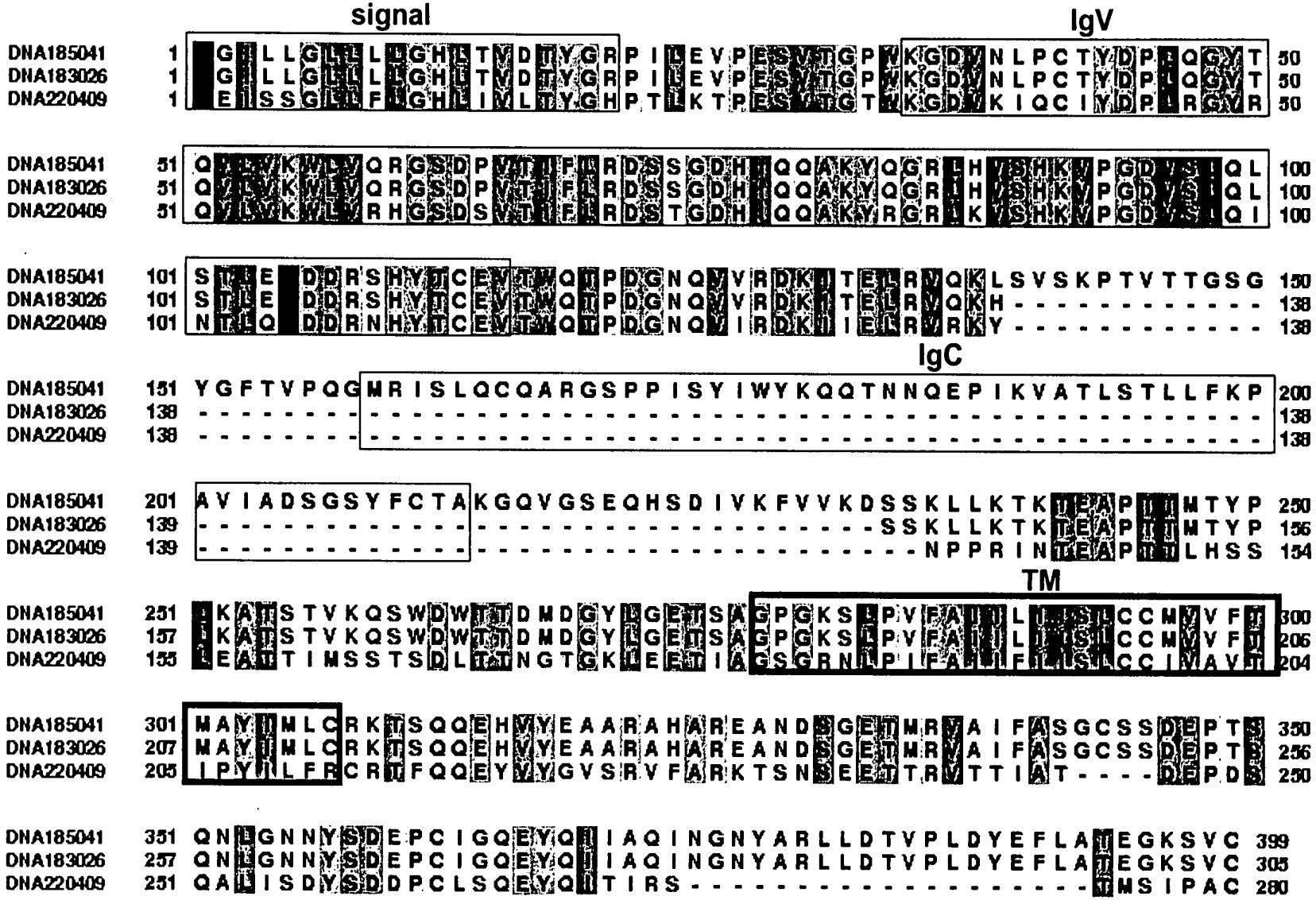

FL-1 Height
40
35
30
25
20
15
10
5
0
Buffer only
+ huJAM.Fc
+ Pro362.Fc
+ His Control
+ Pro1868.His
+ Mouse IgG
+ 12D10.2F9
10 µg/mL
Pro1868.His
5 µg/mL +
Pro245 CHO

Figure 55


100
80
60
40
20
0
Mean FL-1 over Unstained Control
mAb 12D10.2F9
mAb 10A5
Mouse IgG
CHO-JI
CuL8r
Ctl CHO



Murine STIgMA on X-chromosome
Human STIgMA on X-chromosome

Fig. 56

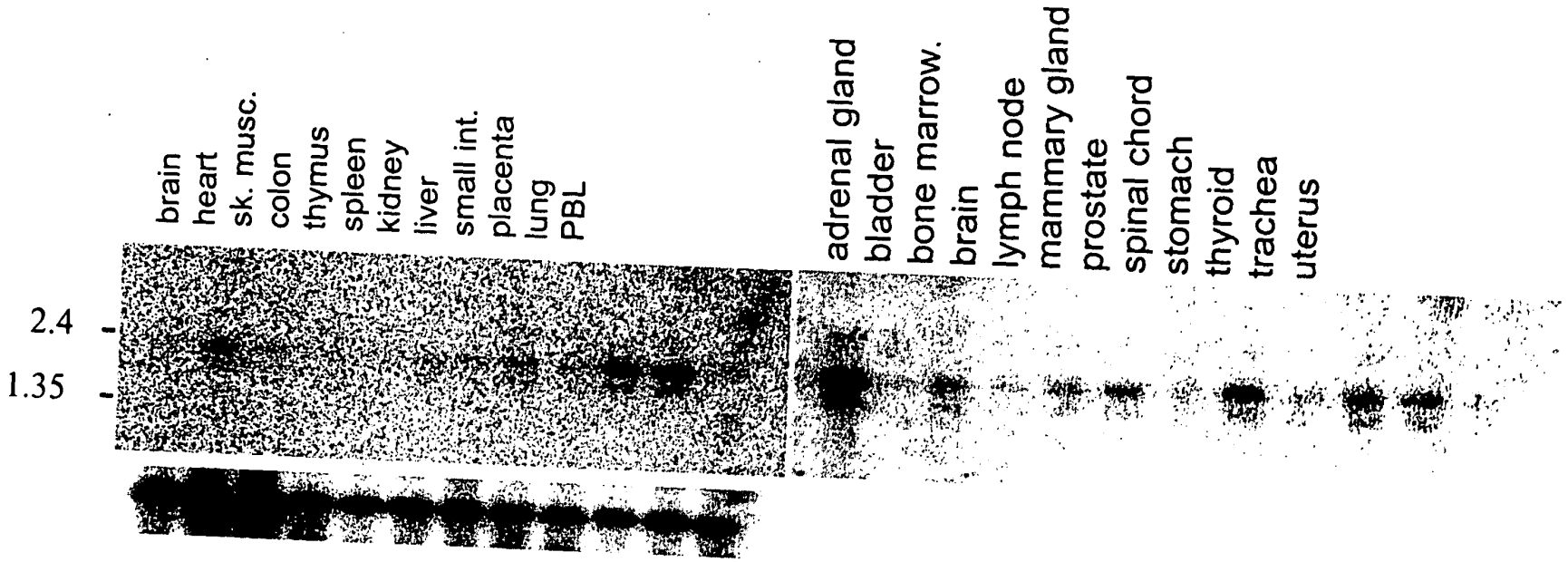

brain
heart
sk. musc.
colon
thymus
spleen
kidney
liver
small int.
placenta
lung
PBL
adrenal gland
bladder
bone marrow.
brain
lymph node
mammary gland
prostate
spinal chord
stomach
thyroid
trachea
uterus
2.4
1.35

Fig. 57

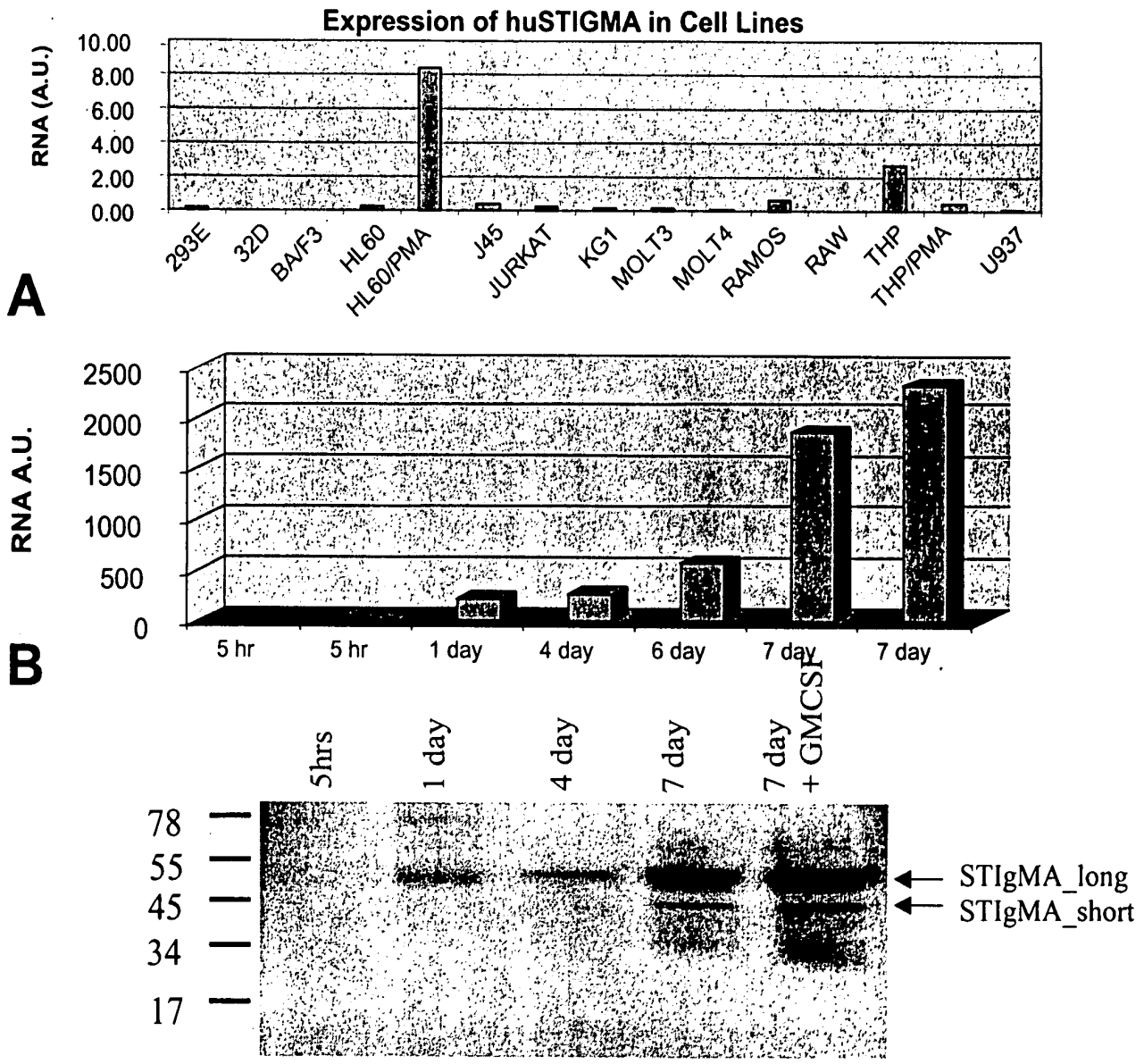

Expression of huSTIGMA in Cell Lines
RNA (A.U.)
10.00
8.00
6.00
4.00
2.00
0.00
293E
32D
BA/F3
HL60
HL60/PMA
J45
JURKAT
KG1
MOLT3
MOLT4
RAMOS
RAW
THP
THP/PMA
U937
A
RNA A.U.
2500
2000
1500
1000
500
0
5 hr
5 hr
1 day
4 day
6 day
7 day
7 day
B
5hrs
1 day
4 day
7 day
7 day + GMCSF
78
55
45
34
17
STIgMA_long
STIgMA_short
C

Fig. 58

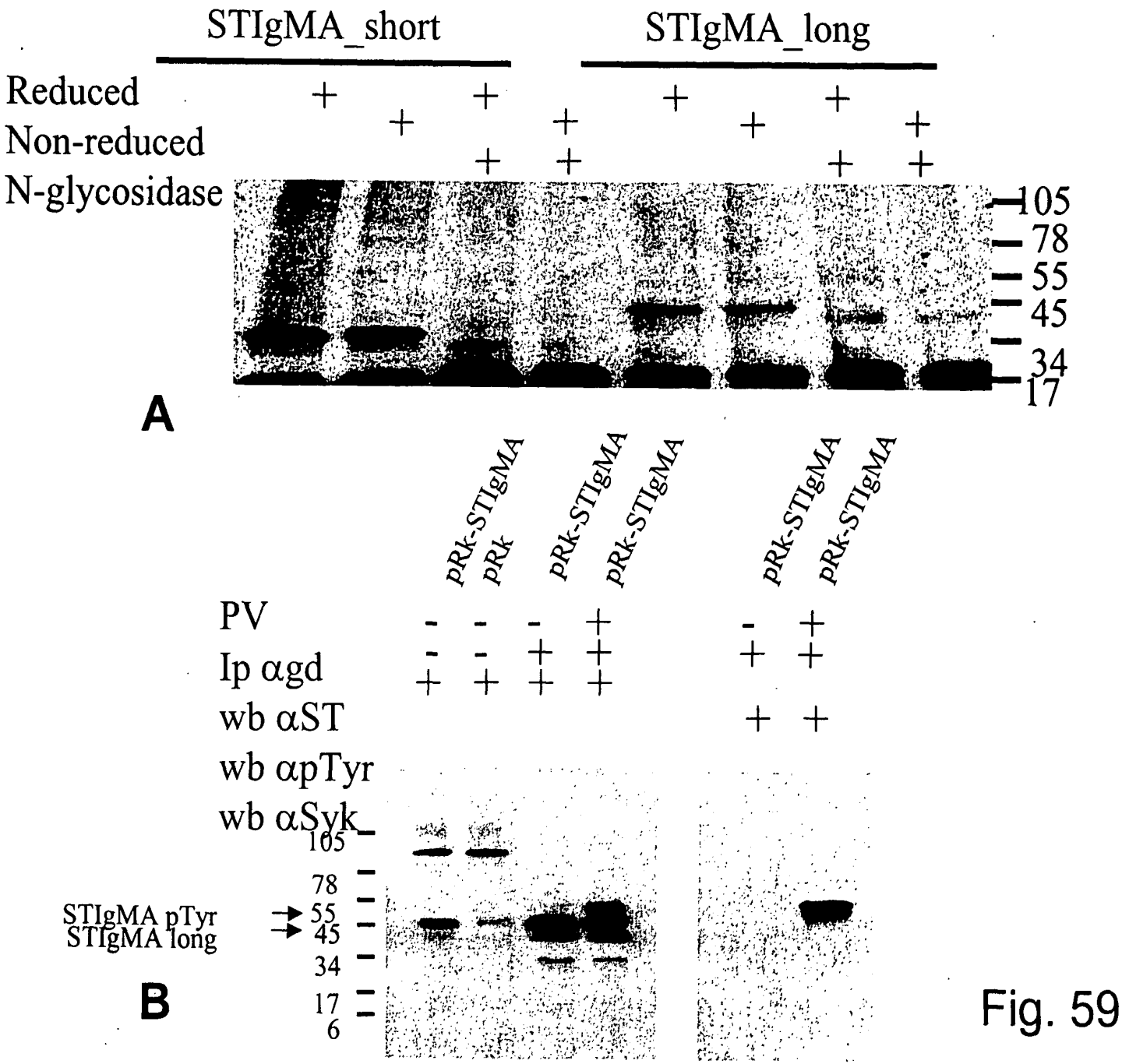

STIgMA_short
STIgMA_long
Reduced
Non-reduced
N-glycosidase
105
78
55
45
34
17
A
pRk-STIgMA
pRk
pRk-STIgMA
pRk-STIgMA
pRk-STIgMA
pRk-STIgMA
PV
Ip αgd
wb αST
wb αpTyr
wb αSyk
105
78
55
45
34
17
6
STIgMA pTyr
STIgMA long
B

Fig. 59

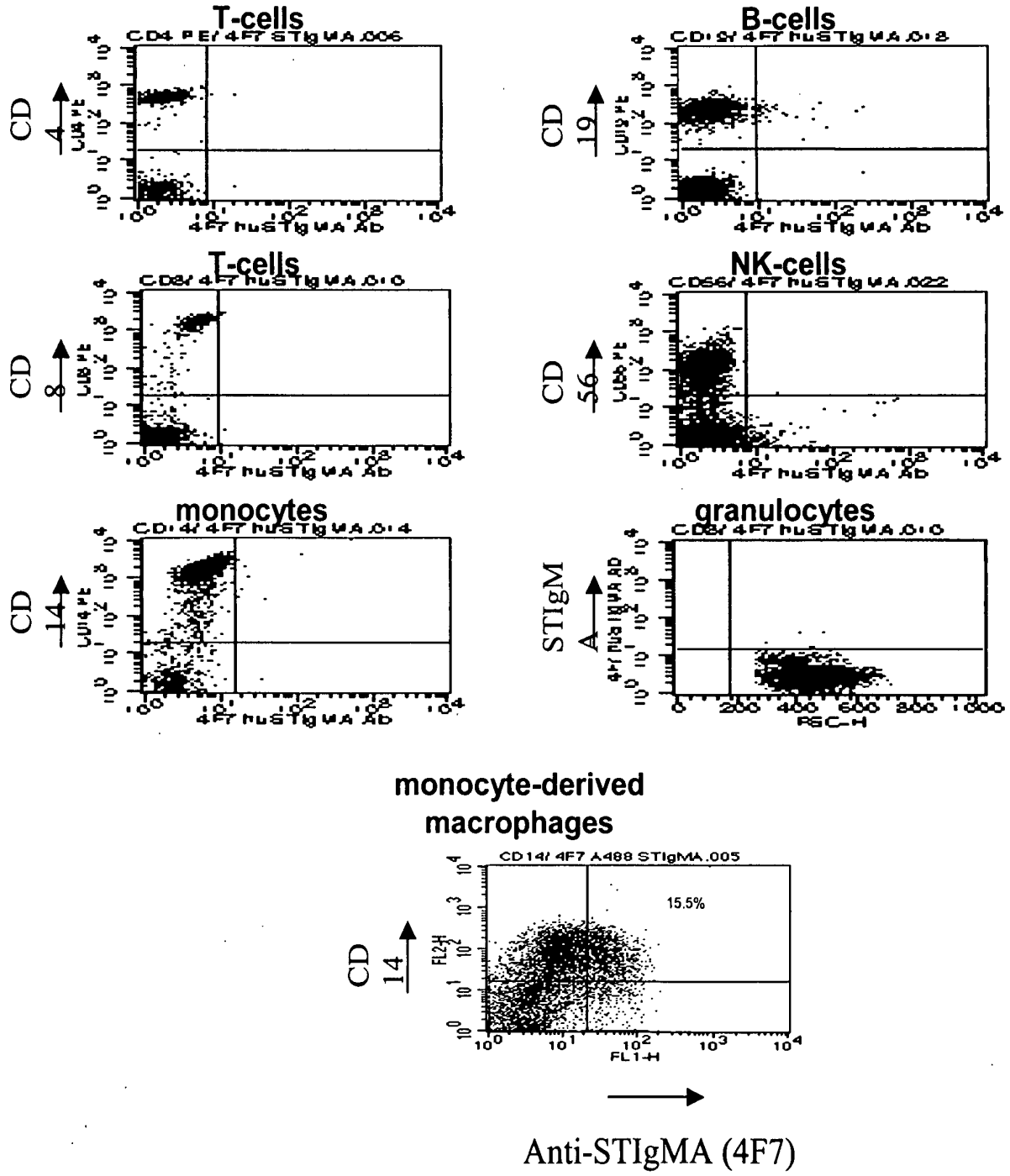

T-cells
CD 4
T-cells
CD 8
monocytes
CD 14
B-cells
CD 19
NK-cells
CD 56
granulocytes
STIgM
monocyte-derived
macrophages
CD14/ 4F7 A488 STIgMA .005
15.5%
CD 14
FL2-H
FL1-H
Anti-STIgMA (4F7)

Fig. 60

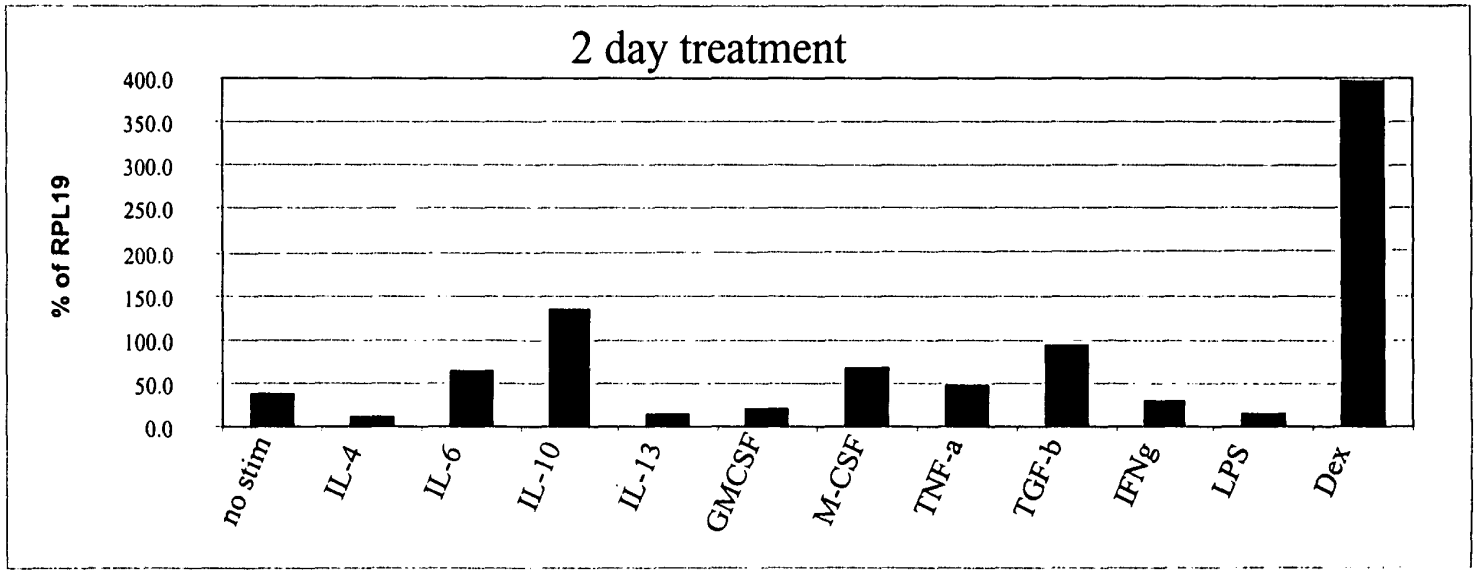

2 day treatment
% of RPL19
400.0
350.0
300.0
250.0
200.0
150.0
100.0
50.0
0.0
no stim
IL-4
IL-6
IL-10
IL-13
GMCSF
M-CSF
TNF-a
TGF-b
IFNg
LPS
Dex

Fig. 61A

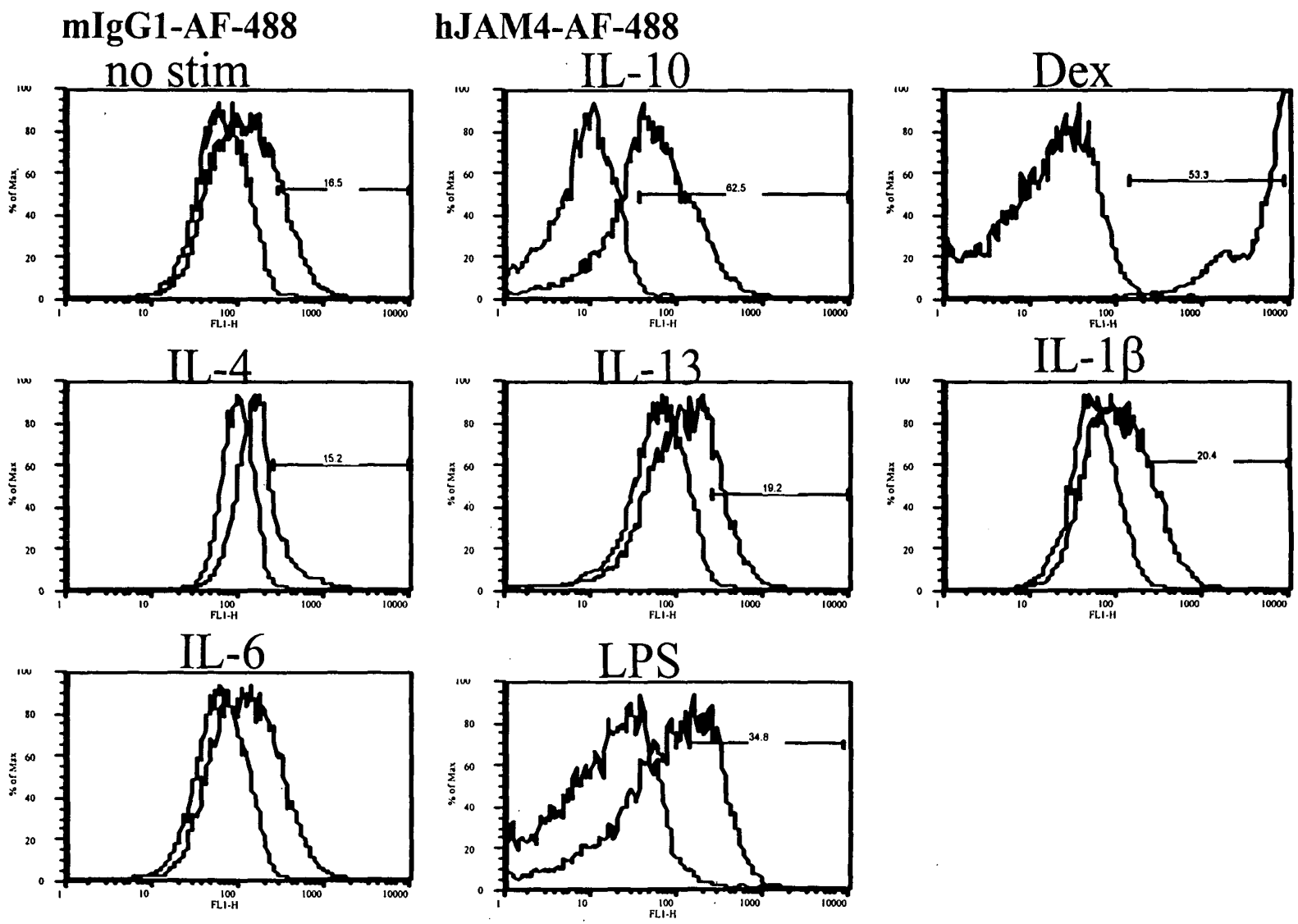

mIgG1-AF-488
hJAM4-AF-488
no stim
IL-10
Dex
IL-4
IL-13
IL-1β
IL-6
LPS
% of Max
FL1-H
16.5
62.5
53.3
15.2
19.2
20.4
34.8

Fig. 61B

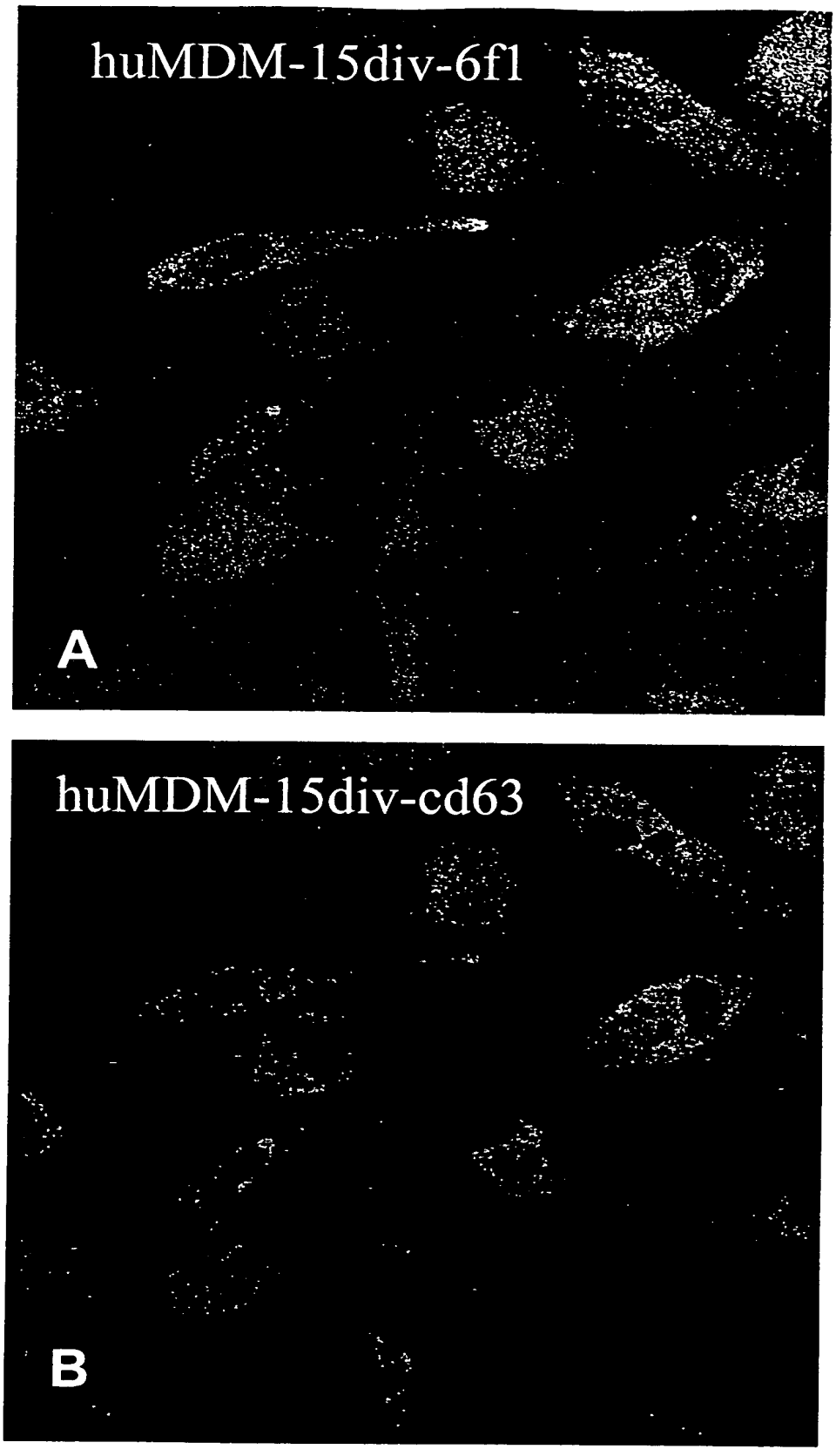


Fig.62

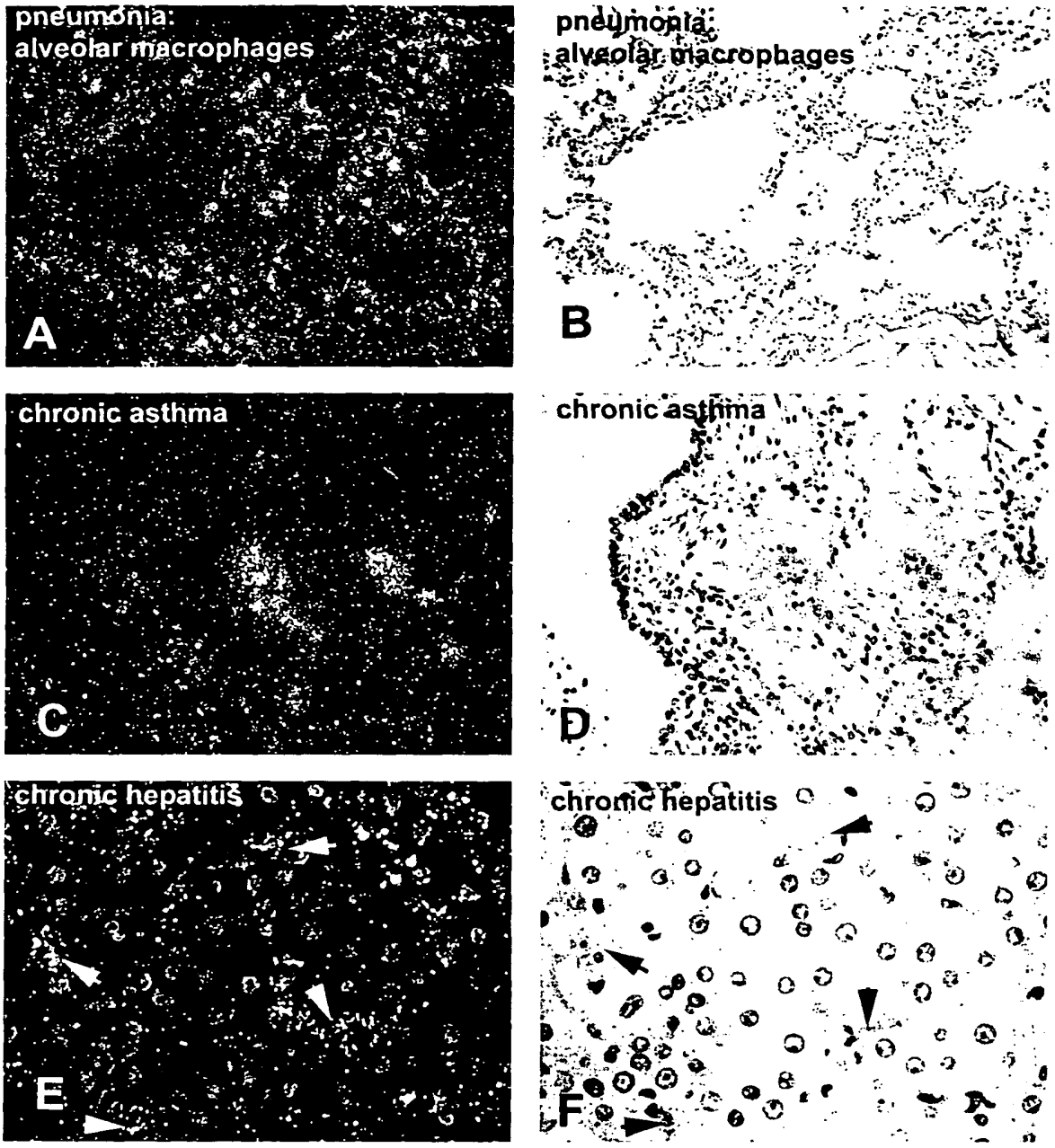

pneumonia:
alveolar macrophages
A
pneumonia:
alveolar macrophages
B
chronic asthma
C
chronic asthma
D
chronic hepatitis
E
chronic hepatitis
F

Fig. 63

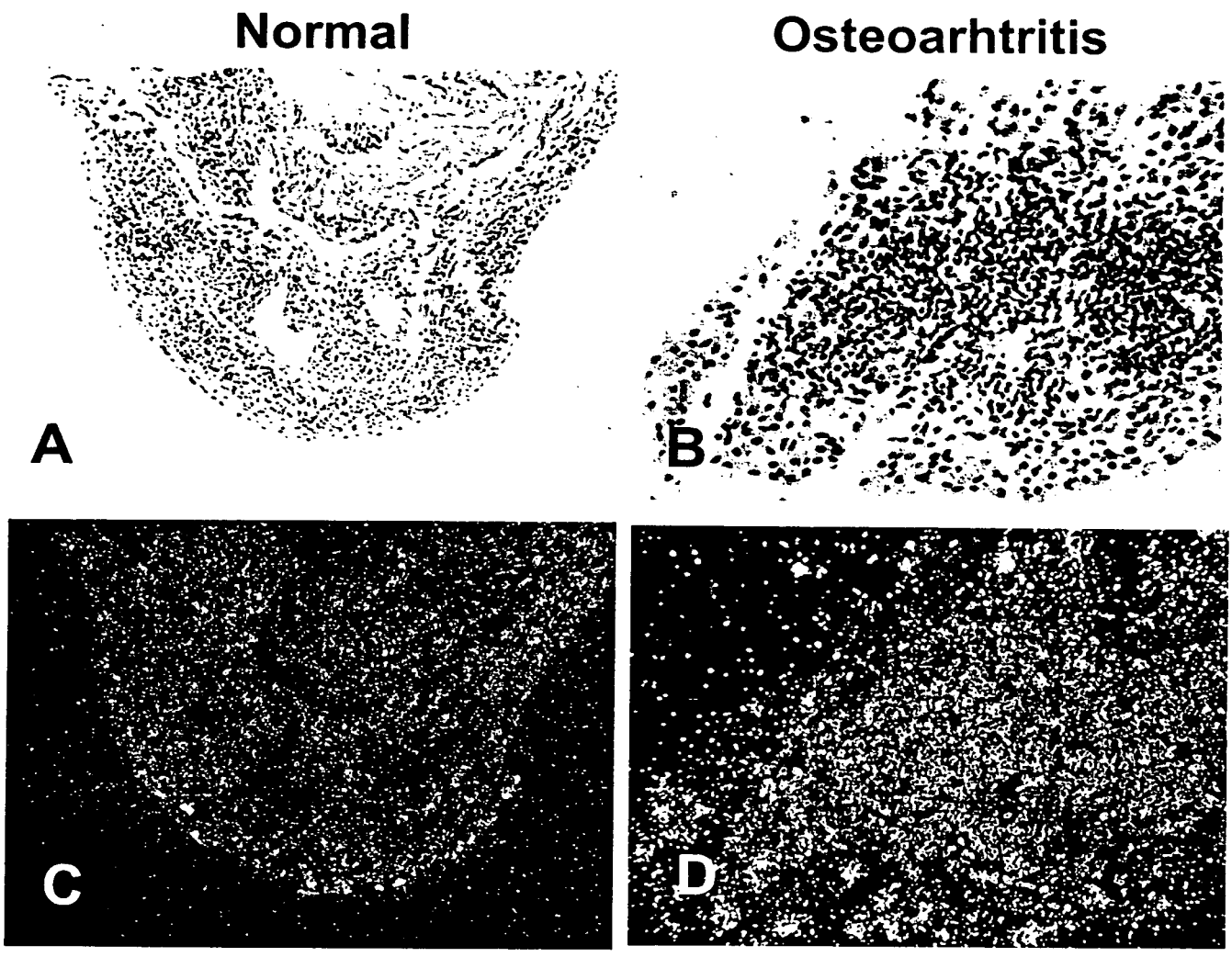


Fig. 64

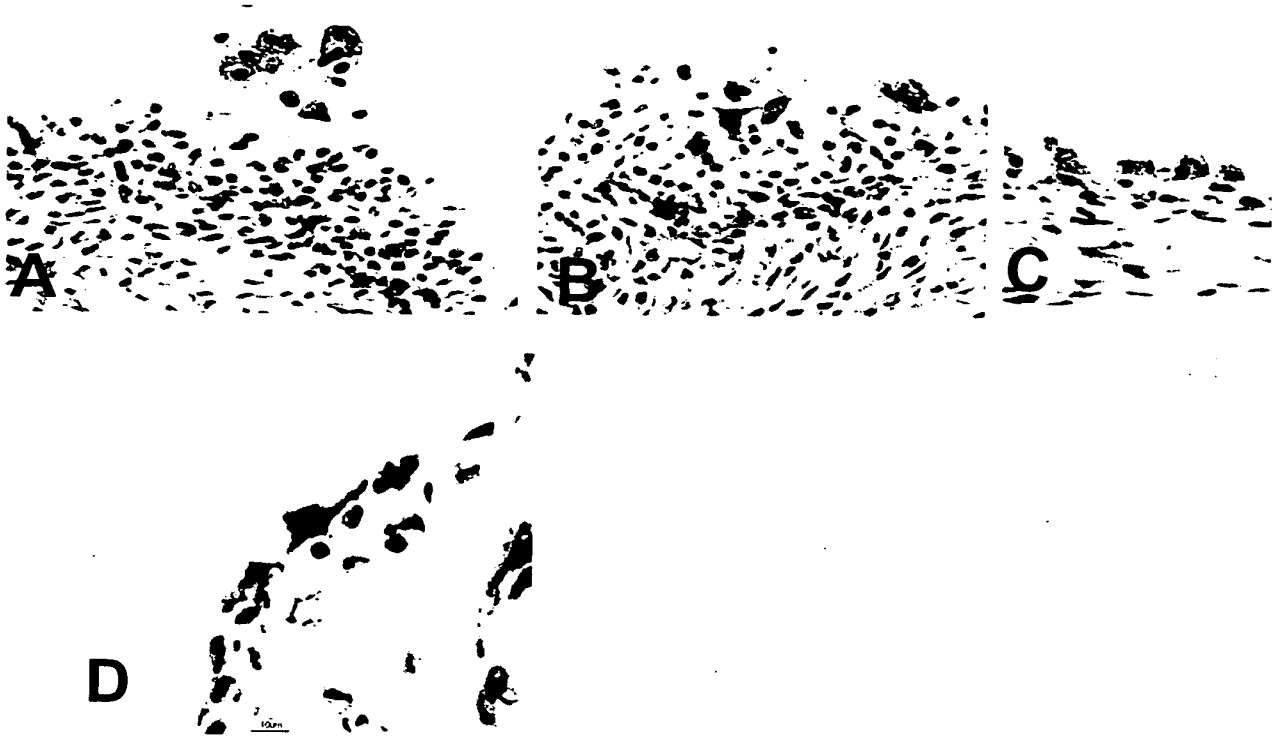


Fig. 65

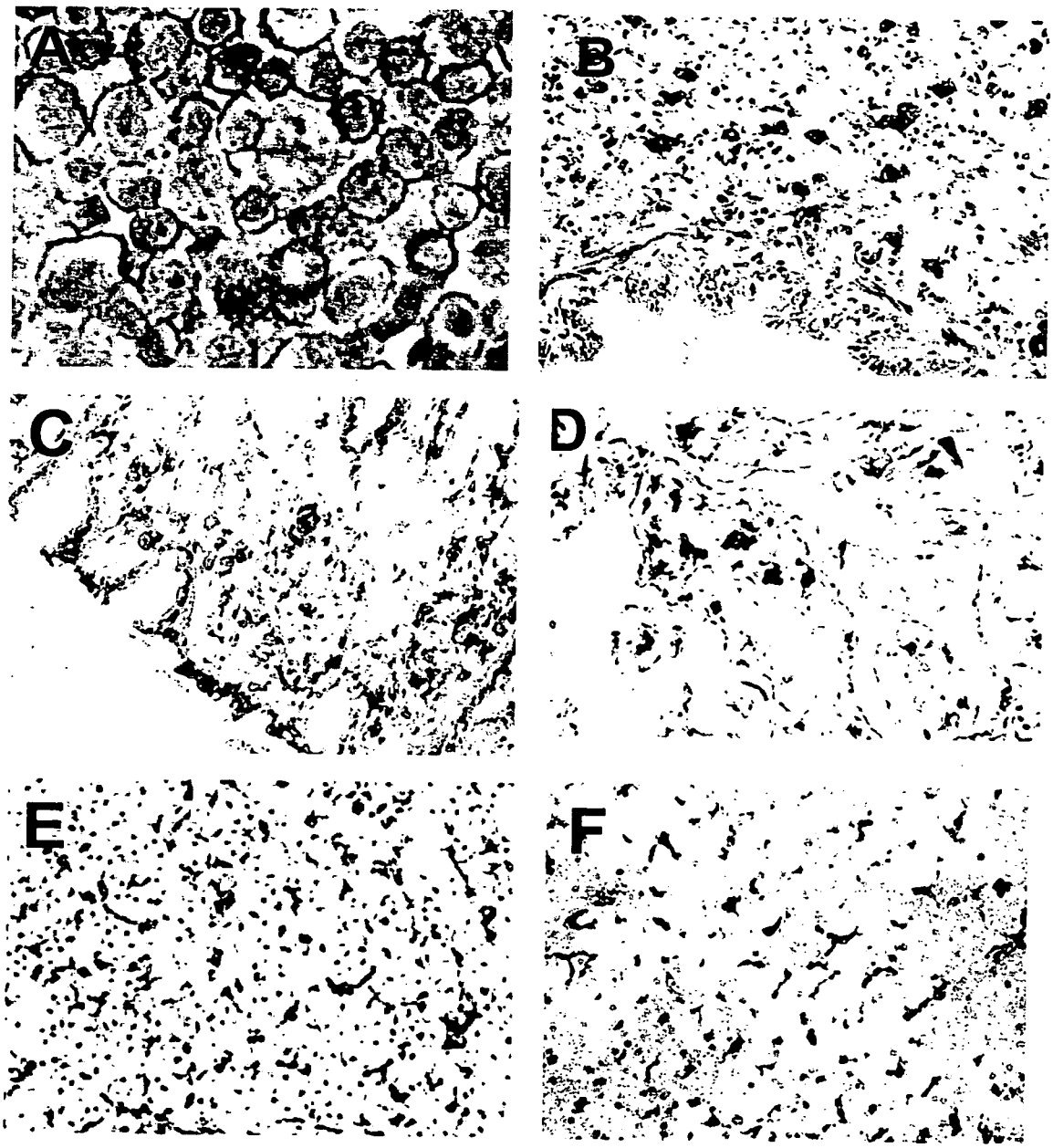


Fig. 66

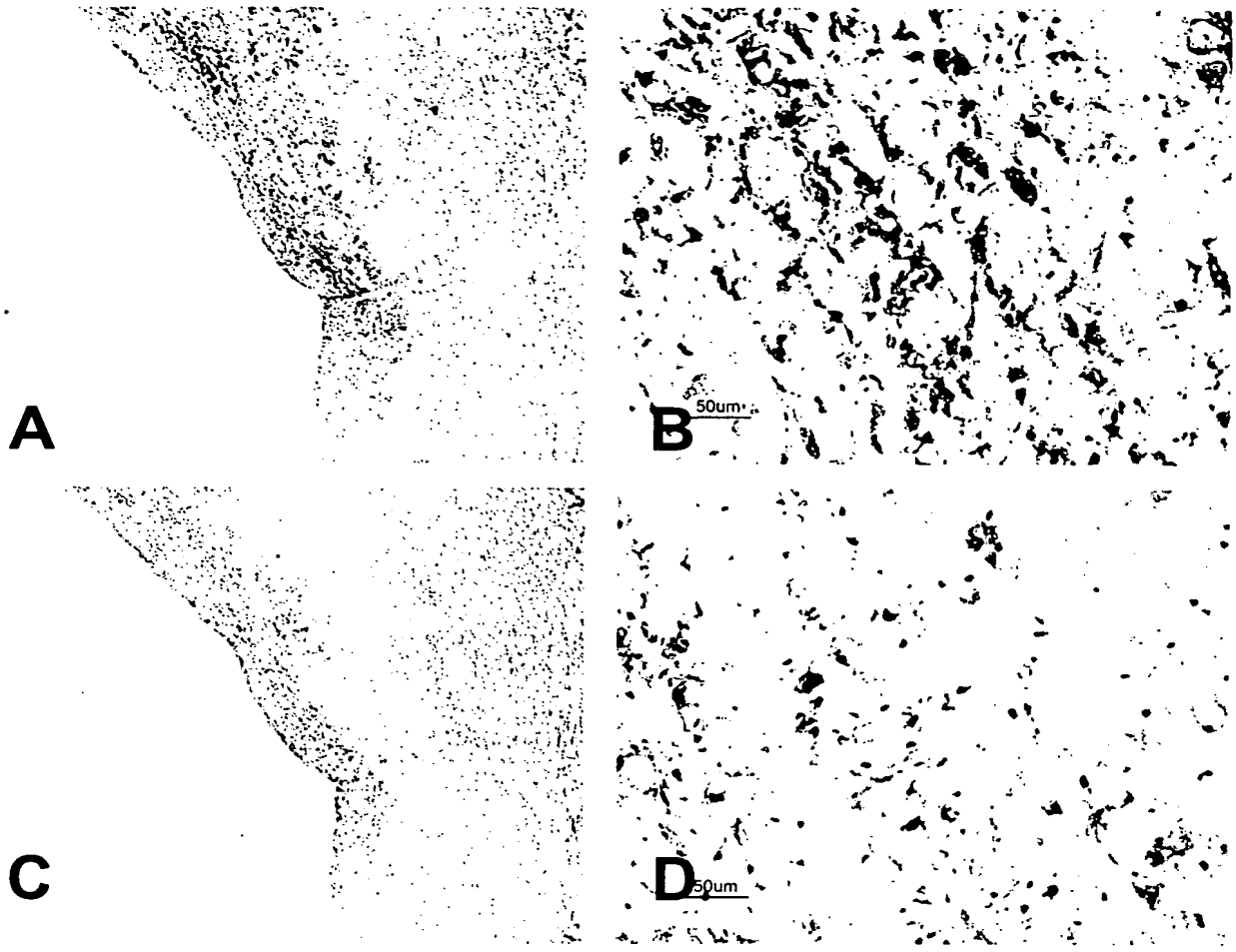


Fig. 67

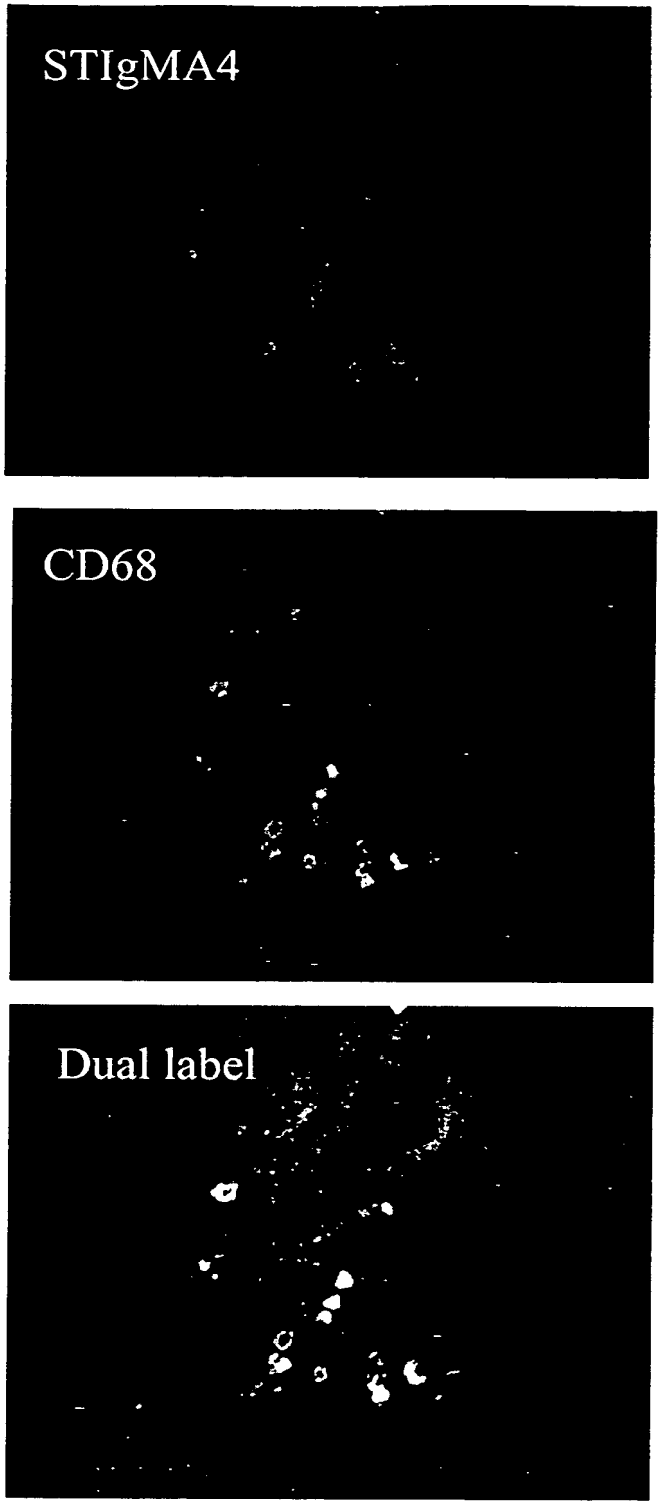


Fig. 68

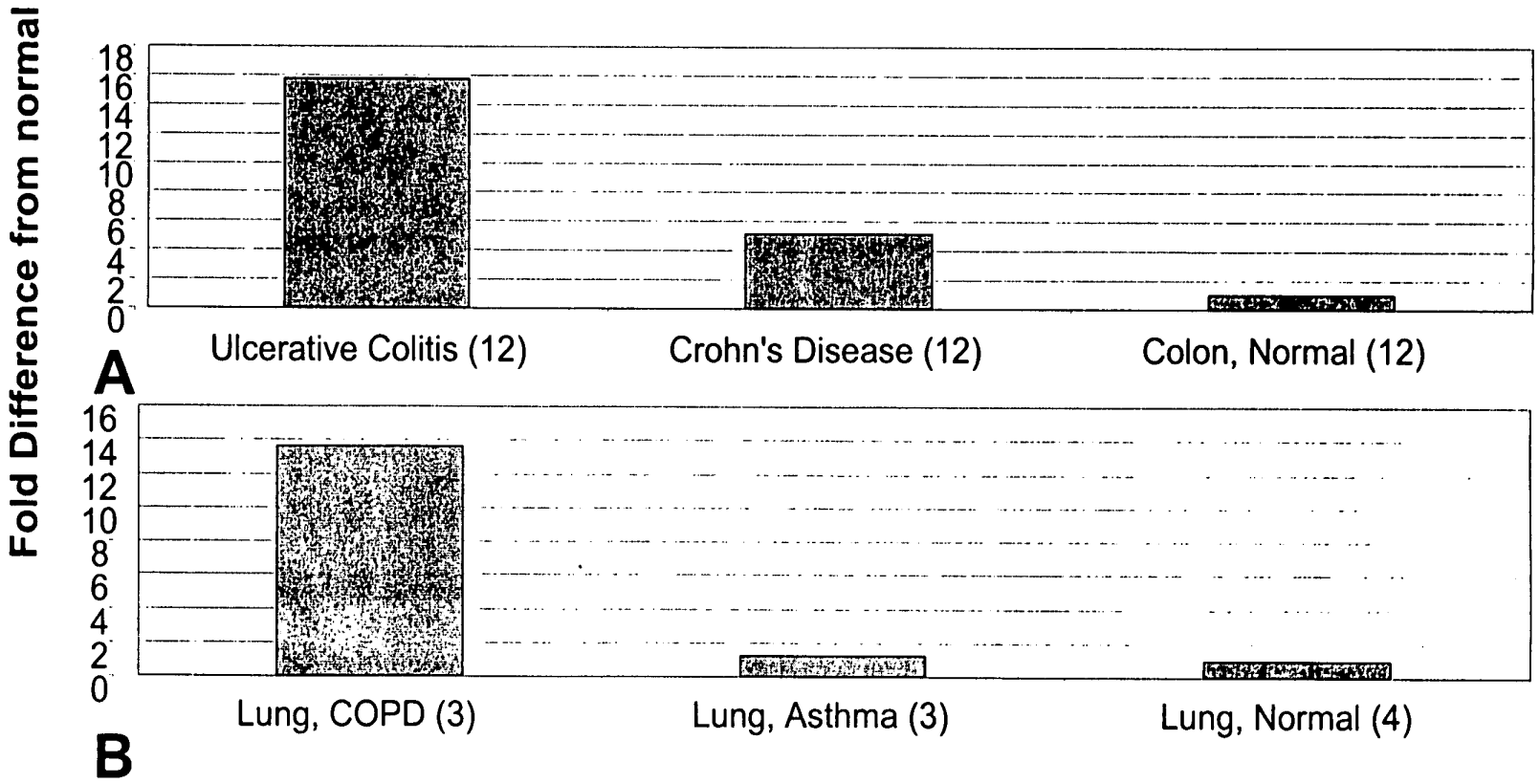
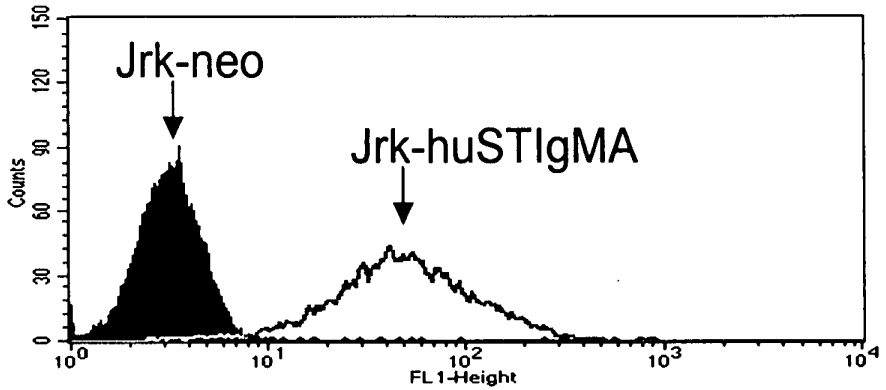
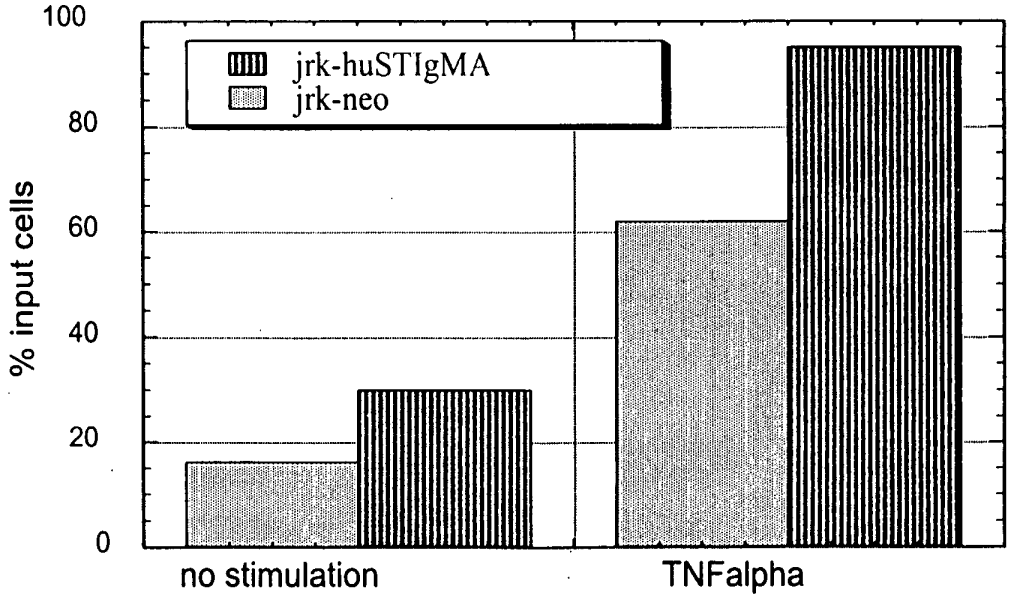

Fold Difference from normal
18
16
14
12
10
8
6
4
2
0
Ulcerative Colitis (12)
Crohn's Disease (12)
Colon, Normal (12)
A
16
14
12
10
8
6
4
2
0
Lung, COPD (3)
Lung, Asthma (3)
Lung, Normal (4)
B

Fig 69


Jrk-neo
Jrk-huSTIgMA
Counts
FL1-Height

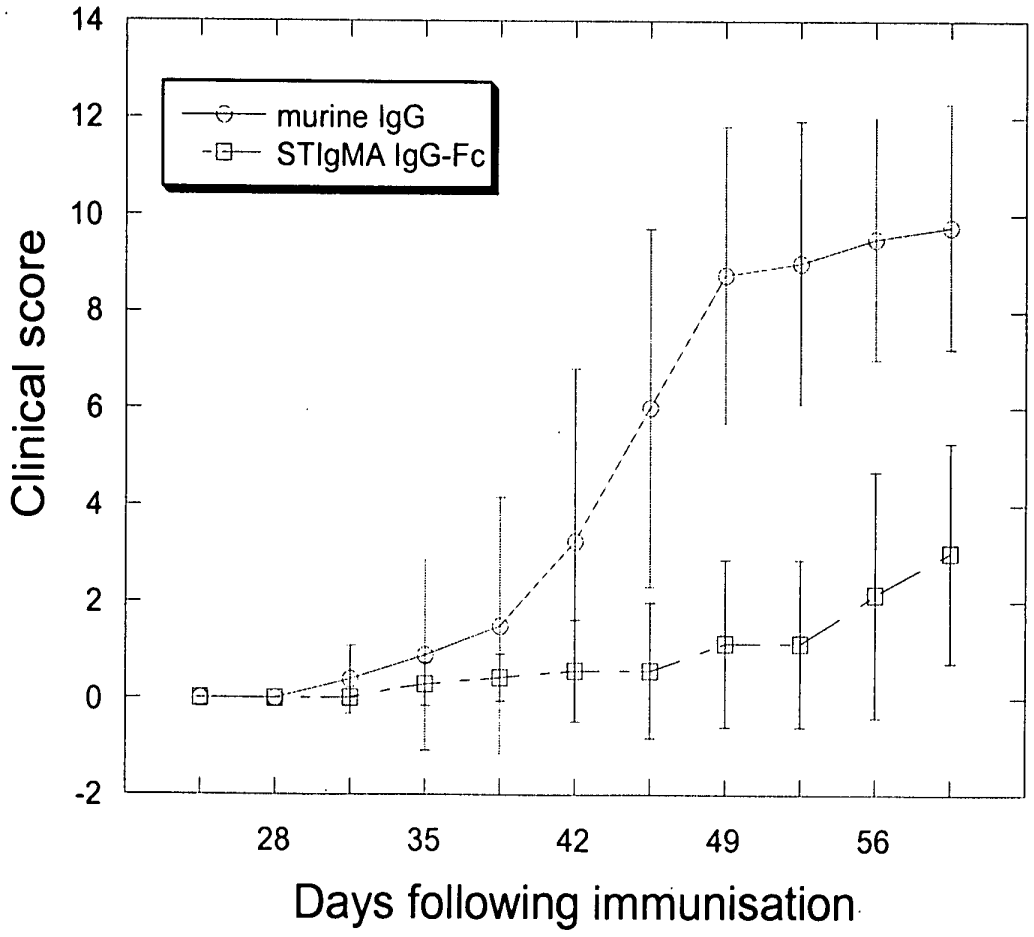
A


jrk-huSTIgMA
jrk-neo
% input cells
no stimulation
TNFalpha

B

Fig 70

Figure 71: Effect of Systemic Injection of muSTIgMA-Fc on the Progression of CIA



t-test

p-value = .0004 for IgG1 vs. muSTIgMA

This p-value has been (very) conservatively adjusted for multiple comparisons (Bonferroni adjustment: 2*p-value since there are two comparisons being performed)

Plots indicate mean $\pm$ SD